

PT primary hyperthyroidism and osteoporosis
 XX
 PS Claim 4; Page 18; 56pp; English.
 XX
 CC Interleukin-18 (IL-18) or a functional equivalent can be used for
 CC inhibition of osteoclast formation. IL-18 is used for treating or
 CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
 CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
 CC arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and
 CC osteoporosis.
 XX
 SQ Sequence 157 AA;

Query Match 100.0%; Score 816; DB 19; Length 157;
 Best Local Similarity 100.0%; Pred. No. 1.2e-83;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSCDRNAPRTIFTIISMYSKDSQPRGM 60
 DB 1 yfgklesklsvirnlndqvlfidqgnrplfedmtsdscdrdnprtifiismyskdsqprgm 60
 QY 61 AVTISVCKEISTLSCENKIISFKEMPPDNKDKSDIIFQRSVPGHDKMKQFESSY 120
 DB 61 avtislsvckekistlscenkliisfkemppdnkdkdsdliifqrsvpgdhdkmkqfessy 120
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
 DB 121 egyflacekerdlfklllkkedelgdrsimftvqned 157

RESULT 2
 AAY57570
 ID AAY57570 standard; protein; 157 AA.
 XX
 AC AAY57570;
 XX
 DT 06-MAR-2000 (first entry)
 XX
 DE Human interleukin 18 protein sequence SEQ ID NO:1.
 XX
 KW Human; Interleukin 18; IL-18; potentiator; IGIF; tumour; cancer;
 KW Interferon-gamma-inducing factor; growth inhibition; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO959565-A1.
 XX
 PD 25-NOV-1999.
 XX
 PF 20-MAY-1999; 99WO-US11160.
 XX
 PR 21-MAY-1998; 98US-0086560.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Johnson RK;
 XX
 DR WPI; 2000-062368/05.
 XX
 PT New polypeptides, useful for preparation of composition for preventing
 PT and/or treating cancer by inhibiting tumor growth -
 XX
 PS Claim 1; Page 49-50; 53pp; English.
 XX

CC The present sequence represents human interleukin 18 (IL-18). The
 CC present invention describes a compound comprising human or murine IL-18
 CC in combination with a chemotherapeutic agent (I). Also described are:
 CC (1) a method of preventing and/or treating cancer in a mammal comprising
 CC the administration of a cancer inhibiting amount of (I) comprising the
 CC IL-18 protein and the chemotherapeutic agent and optionally a
 CC pharmaceutically acceptable carrier; and (2) a method of inhibiting the
 CC growth of tumour cells in a mammal sensitive to a composition comprising

CC human IL-18 and/or murine IL-18 and the chemotherapeutic agent (and
 CC optionally a pharmaceutically acceptable carrier), comprising
 CC administering to a mammal afflicted with the tumour cells an effective
 CC tumour cell growth inhibiting amount of (I). The IL-18 protein in
 CC conjunction with a chemotherapeutic agent is useful in a method for
 CC preventing and/or treating cancer in mammals by inhibiting the growth
 CC of tumours or cancerous cells in mammals.
 XX
 SQ Sequence 157 AA;

Query Match 100.0%; Score 816; DB 21; Length 157;
 Best Local Similarity 100.0%; Pred. No. 1.2e-83;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSCDRNAPRTIFTIISMYSKDSQPRGM 60
 DB 1 yfgklesklsvirnlndqvlfidqgnrplfedmtsdscdrdnprtifiismyskdsqprgm 60
 QY 61 AVTISVCKEISTLSCENKIISFKEMPPDNKDKSDIIFQRSVPGHDKMKQFESSY 120
 DB 61 avtislsvckekistlscenkliisfkemppdnkdkdsdliifqrsvpgdhdkmkqfessy 120
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
 DB 121 egyflacekerdlfklllkkedelgdrsimftvqned 157

RESULT 3
 AAE06661
 ID AAE06661 standard; protein; 157 AA.
 XX
 AC AAE06661;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Human interleukin-1gamma (IL-1gamma) protein.
 XX
 KW Human; Interleukin-1gamma; IL-1gamma; virucide; hepatotropic; fever;
 KW immunological disorder; tumour; inflammatory disorder; hypoglycaemia;
 KW autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;
 KW psoriasis; viral infection; allergy; cytokine; HIV; drug screening.
 XX
 OS Homo sapiens.
 XX
 PN WO200157219-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 01-FEB-2001; 2001WO-US03285.
 XX
 PR 02-FEB-2000; 2000US-0179638.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 PI Debets JEMA, Timans JC, Bazan JF, Kastelein RA;
 XX
 DR WPI; 2001-488886/53.
 XX

PT Novel isolated or recombinant antigenic interleukin-1 delta or epsilon
 PT polypeptide useful for treating conditions exhibiting abnormal
 PT expression of interleukin such as immunological disorders, tumor and
 PT allergy -
 XX
 PS Disclosure; Fig 1; 103pp; English.
 XX
 CC The invention relates to recombinant antigenic Interleukin-1 like
 CC molecules and their corresponding nucleic acid sequences, designated
 CC as interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon).
 CC IL-1delta and IL-1epsilon are useful for treating conditions exhibiting
 CC abnormal expression of the interleukin such as immunological disorders,
 CC tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis,
 CC allergy, autoimmune diseases and infectious diseases (e.g., pulmonary

CC tuberculosis, leprosy, fulminant hepatitis, and viral infections such as
 CC HTV). The invention also relates to methods of using the composition
 CC containing IL-delta or IL-lepsilon for both diagnostic and therapeutic
 CC utilities. IL-delta is used as an immunogen for the production of
 CC antisera or antibodies specific, e.g., capable of distinguishing between
 CC IL-1 family members and an IL-delta, for the interleukin or its
 CC fragment. The purified interleukin is used as a reagent to detect any
 CC antibodies generated in response to the presence of elevated levels of
 CC expression, or immunological disorders which lead to antibody production
 CC to the endogenous cytokine. The invention also contemplates the use of
 CC competitive drug screening assays. The present sequence is human
 CC interleukin-1gamma (IL-1gamma) protein related to the invention.
 XX
 SQ Sequence 157 AA;

Query Match 100.0%; Score 816; DB 22; Length 157;
 Best Local Similarity 100.0%; Pred. No. 1.2e-83;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIIFIIMYKDSQPRGM 60
 DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIIFIIMYKDSQPRGM 60
 QY 61 AVTISVKCEKISTLSCEKNIISFKEMNPPDNIKDKSDIIFFORSVPGHDKNQFESSY 120
 DB 61 AVTISVKCEKISTLSCEKNIISFKEMNPPDNIKDKSDIIFFORSVPGHDKNQFESSY 120
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
 DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 4
 AAG65294
 ID AAG65294 standard; protein; 157 AA.
 XX
 AC AAG65294;
 XX
 DT 30-NOV-2001 (first entry)
 XX
 DE Human interleukin-18 (IL-18) protein fragment.
 XX
 KW IL-18; Interleukin-18; human; antibody; antirheumatic; cerebroprotective;
 KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
 KW immunosuppressive; antidepressant; neuroleptic; hepatotropic.
 XX
 OS Homo sapiens.
 XX
 PN WO200158956-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US04170.
 XX
 PR 10-FEB-2000; 2000US-0181608.
 XX
 PA (BADI) BASF AG.
 XX
 PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
 PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrocks CP, Thompson JB;
 PI Lennard SN;
 DR WPI; 2001-550020/61.
 XX
 PT Novel antibodies and compounds capable of binding to human
 PT interleukin-18 useful for treating, e.g., inflammatory disorders,
 PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -
 XX
 PS Disclosure; Page 9; 91pp; English.
 XX
 CC The invention provides isolated antibodies, or antigen-binding portions,

CC that are capable of binding to human interleukin-18 (IL-18). The
 CC antibodies may be used to inhibit human IL-18 activity in, and treat a
 CC disorder where IL-18 is detrimental in, a human subject suffering from,
 CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
 CC inflammatory bowel disease, and osteoarthritis), neurological disorders
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
 CC stroke), heart failure, myocardial infarction, autoimmune diseases such
 CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
 CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
 CC antibody may occur before, concurrent, or after administration of a
 CC second agent selected from an antibody, or fragment, capable of binding
 CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
 CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
 CC agents. The present sequence represents a human IL-18 protein fragment.
 XX
 SQ Sequence 157 AA;

Query Match 100.0%; Score 816; DB 22; Length 157;
 Best Local Similarity 100.0%; Pred. No. 1.2e-83;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIIFIIMYKDSQPRGM 60
 DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIIFIIMYKDSQPRGM 60
 QY 61 AVTISVKCEKISTLSCEKNIISFKEMNPPDNIKDKSDIIFFORSVPGHDKNQFESSY 120
 DB 61 AVTISVKCEKISTLSCEKNIISFKEMNPPDNIKDKSDIIFFORSVPGHDKNQFESSY 120
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
 DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 5
 AAG65351
 ID AAG65351 standard; protein; 157 AA.
 XX
 AC AAG65351;
 XX
 DT 30-NOV-2001 (first entry)
 XX
 DE Human interleukin-18 (IL-18) protein fragment.
 XX
 KW IL-18; Interleukin-18; human; antibody; antirheumatic; cerebroprotective;
 KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
 KW immunosuppressive; antidepressant; neuroleptic; hepatotropic.
 XX
 OS Homo sapiens.
 XX
 PN WO200158956-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US04170.
 XX
 PR 10-FEB-2000; 2000US-0181608.
 XX
 PA (BADI) BASF AG.
 XX
 PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
 PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrocks CP, Thompson JB;
 PI Lennard SN;
 DR WPI; 2001-550020/61.
 XX
 PT Novel antibodies and compounds capable of binding to human
 PT interleukin-18 useful for treating, e.g., inflammatory disorders,
 PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -
 XX
 PS Disclosure; Page 14; 91pp; English.

XX The invention provides isolated antibodies, or antigen-binding portions,
 CC that are capable of binding to human interleukin-18 (IL-18). The
 CC antibodies may be used to inhibit human IL-18 activity in, and treat a
 CC disorder where IL-18 is detrimental in, a human subject suffering from,
 CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
 CC inflammatory bowel disease, and osteoarthritis), neurological disorders
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
 CC stroke), heart failure, myocardial infarction, autoimmune diseases such
 CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
 CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
 CC antibody may occur before, concurrent, or after administration of a
 CC second agent selected from an antibody, or fragment, capable of binding
 CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
 CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
 CC agents. The present sequence represents a human IL-18 protein fragment.
 XX Sequence 157 AA;

Query Match 100.0%; Score 816; DB 22; Length 157;
 Best Local Similarity 100.0%; Pred. No. 1.2e-83;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNNDQVLFIDQGNRPFLFEDMTSDCRDNPRTFIISMYKDSQPRGM 60
 Db 1 yfgklesklsvirnndqvlfidqgnrplfedmtsdcrdnprtfiismykdsqprgm 60
 QY 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNKDKTSIIFFQRSVPGHDKMQFESSY 120
 Db 61 avtisvkcekistlscenkliisfkemppdnkdktsdiiffqrsvpghdnkmqfessy 120
 QY 121 EGYFLACERKDLFKLILKKEDELGDRSIMFTVQNEH 157
 Db 121 egyflacekerdlfkliikkedelgdrsimftvqned 157

RESULT 6
 AAY85167
 ID AAY85167 standard; Protein; 158 AA.
 XX AAY85167;
 XX 23-JUN-2000 (first entry)
 DE Human interleukin-18 (IL-18) amino acid sequence.
 XX Interleukin-18; production; IL-18; human; medical injection product.
 KW Homo sapiens.
 OS CN1243130-A.
 PN 02-FEB-2000.
 PD 24-JUL-1998; 98CN-0103307.
 PF 24-JUL-1998; 98CN-0103307.
 PR (WUGG/) WU G.
 XX Wu G, Liu Z;
 PI WPI: 2000-340020/30.
 DR N-PSDB; AAA10526.

XX Preparation method for engineering bacteria for recombination of human
 CC interleukin-18 and its product thereof -
 PS Claim 1; Page 2; 17pp; English.
 XX This sequence represents the human interleukin-18 (IL-18) amino acid
 CC sequence. The invention relates to a method for engineering bacterium for

CC recombination of human IL-18 and a method for the preparation of IL-18. A
 CC primer containing a restriction endonuclease site can be used to
 CC accurately obtain the IL-18 gene containing 474 nucleotides, and uses the
 CC stop codon preferred by coli bacillus to raise the expression rate. The
 CC method uses a high-amplification culture medium to increase the
 CC expression level and only requires a one-step purification process to
 CC obtain a medical injection-pure product.
 XX Sequence 158 AA;

Query Match 100.0%; Score 816; DB 21; Length 158;
 Best Local Similarity 100.0%; Pred. No. 1.2e-83;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNNDQVLFIDQGNRPFLFEDMTSDCRDNPRTFIISMYKDSQPRGM 60
 Db 1 yfgklesklsvirnndqvlfidqgnrplfedmtsdcrdnprtfiismykdsqprgm 61
 QY 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNKDKTSIIFFQRSVPGHDKMQFESSY 120
 Db 62 avtisvkcekistlscenkliisfkemppdnkdktsdiiffqrsvpghdnkmqfessy 121
 QY 121 EGYFLACERKDLFKLILKKEDELGDRSIMFTVQNEH 157
 Db 122 egyflacekerdlfkliikkedelgdrsimftvqned 158

RESULT 7
 AAW48959
 ID AAW48959 standard; Peptide; 180 AA.
 XX AAW48959;
 XX 25-SEP-1998 (first entry)
 DE Wild-type human interferon-gamma inducing factor.
 KW Interferon-gamma inducing factor; interferon-gamma; killer cell;
 KW antitumour agent; antiviral agent; antimicrobial agent; tumour; IGIF;
 KW hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;
 KW osteoporosis; thrombopenia; acquired immunodeficiency syndrome.
 OS Homo sapiens.
 EH Key Location/Qualifiers
 FT Peptide 1..23
 FT Protein /note= "Signal peptide"
 FT /note= "Mature human IGIF which is claimed by the
 inventors under claim 3 in the specification"

PN EP845530-A2.
 XX 03-JUN-1998.
 PD 28-NOV-1997; 97EP-0309632.
 PF 14-NOV-1997; 97JP-0329715.
 PR 29-NOV-1996; 96JP-0333037.
 PR 21-JAN-1997; 97JP-0020906.
 XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX Kurimoto M, Okamoto I, Yamamoto K;
 PI WPI: 1998-288747/26.
 DR N-PSDB; AAV32754.

XX Mutants of interferon-gamma inducing polypeptide - useful as
 CC antitumour, antiviral, antimicrobial or anti-immunopathic agents
 PS Claim 3; pages 36-37; 59pp; English.

XX The present sequence represents the wild-type human interferon-gamma
 CC inducing factor (IGIF). The invention provides for mutant human and
 CC mouse interferon-gamma inducing factors in which one or more cysteine
 CC residues are replaced with different residues at or away from the
 CC consensus sequences shown in AAW48956-W48958. The mutant IGIFs are
 CC capable of stimulating immunocompetent cells for the production of
 CC interferon-gamma and are claimed to be less toxic, more active and
 CC stable than the corresponding wild type IGIF. The mutant IGIFs are also
 CC claimed to enhance killer cell cytotoxicity and/or induce killer cell
 CC formation, and may therefore be useful as antitumour agents, antitumour
 CC immunotherapeutics, antiviral agents and antimicrobial agents. The
 CC mutant IGIFs are also claimed to be useful for treating hepatitis,
 CC acquired immunodeficiency syndrome (AIDS), malaria, tuberculosis, solid
 CC malignant tumours (e.g. renal carcinoma), rheumatism, osteoporosis and
 CC thrombopenia caused by radiation- and chemo-therapy.

XX Sequence 180 AA;

Query Match 100.0%; Score 816; DB 19; Length 180;
 Best Local Similarity 100.0%; Pred. No. 1.5e-83;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYSKDSQPRGM 60
 Db 24 yfgklesklsvirnlndqvlfdqgnrplfedmtsdcrdnprtifiismyskdsqprgm 83
 Qy 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFQSVPGHDNKNMFESSY 120
 Db 84 avtisvkeekistlscenkiisfkemppdnikdtkdsdliifqsvpghdnknmfessy 143
 Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
 Db 144 egyflacekerdlfklllkkeedelgdrsimftvqned 180

RESULT 8
 AAW22047
 ID AAW22047 standard; Protein: 193 AA.
 XX
 AC AAW22047;
 XX
 DT 14-JAN-1998 (first entry)
 XX
 DE Interferon gamma inducing factor-2 (IGIF-2) protein.
 XX
 KW Interferon gamma inducing factor-2; IGIF-2; leucocyte; lymphocyte;
 KW inflammation; proliferation; differentiation; maturation; tissue damage;
 KW human.
 XX
 OS Homo sapiens.
 XX
 PN W09724441-A1.
 XX
 PD 10-JUL-1997.
 XX
 PF 20-DEC-1996; 96WO-US20432.
 XX
 PR 29-DEC-1995; 95US-0580667.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Cocks BG, Coleman R, Hawkins PR;
 XX
 DR WPI; 1997-363677/33.
 DR N-PSDB; AAT74987.
 XX
 XX Novel interferon gamma inducing factor-2 - used to screen for
 PT compounds to diagnose, treat or prevent tissue damage associated
 PT with inflammation
 XX
 PS Claim 1; Page 46; 60pp; English.

XX This is the protein sequence of interferon gamma inducing factor-2
 CC (IGIF-2). An IGIF-2 variant (AAW31757) and an IGIF variant (AAW22049),
 CC which may be an alternate transcript, also exist. Probes derived from
 CC the nucleic acid sequences can be used to quantify the expression of
 CC IGIF-2 in conditions that are associated with inflammation or aberrant
 CC expression of IGIF-2. The protein can be used to screen for compounds
 CC that interact with IGIF-2, such as antibodies, antagonists or other
 CC inhibitors (especially ribozymes or antisense sequences) of IGIF-2
 CC expression or activity. The protein can also be used to diagnose,
 CC prevent or treat IGIF-2 induction of proliferation, differentiation or
 CC maturation of leucocytes or lymphocytes, especially in relation to tissue
 CC damage associated with inflammation.

XX Sequence 193 AA;

Query Match 100.0%; Score 816; DB 18; Length 193;
 Best Local Similarity 100.0%; Pred. No. 1.6e-83;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYSKDSQPRGM 60
 Db 37 yfgklesklsvirnlndqvlfdqgnrplfedmtsdcrdnprtifiismyskdsqprgm 96
 Qy 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFQSVPGHDNKNMFESSY 120
 Db 97 avtisvkeekistlscenkiisfkemppdnikdtkdsdliifqsvpghdnknmfessy 156
 Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
 Db 157 egyflacekerdlfklllkkeedelgdrsimftvqned 193

RESULT 9
 AAW46592
 ID AAW46592 standard; Protein: 193 AA.
 XX
 AC AAW46592;
 XX
 DT 21-MAY-1998 (first entry)
 XX
 DE Amino acid sequence of human interleukin-1-gamma.
 XX
 KW Interleukin-1-gamma; IL-1-gamma; mouse; cytokine; IGIF; interferon-gamma;
 KW induction; antibody; diagnostic assay; fusion protein; activity;
 KW immunological disorder; allergy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 41..47 "beta-1 region"
 FT /note= "beta-1 region"
 FT Region 55..59
 FT /note= "beta-2 region"
 FT Region 64..68
 FT /note= "beta-3 region"
 FT Region 83..88
 FT /note= "beta-4 region"
 FT Region 96..102
 FT /note= "beta-5 region"
 FT Region 108..113
 FT /note= "beta-6 region"
 FT Region 115..120
 FT /note= "beta-7 region"
 FT Region 137..143
 FT /note= "beta-8 region"
 FT Region 147..153
 FT /note= "beta-9 region"
 FT Region 160..164
 FT /note= "beta-10 region"
 FT Region 170..175
 FT /note= "beta-11 region"

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FH Key Location/Qualifiers
FT Cleavage-site 33..36
FT /note= "caspase-8 cleavage site"
XX WO200061768-A2..
XX 19-OCT-2000..
XX 13-APR-2000; 2000WO-IL00220.
XX 13-APR-1999; 99IL-0129427.
XX (YEDA ) YEDA RES & DEV CO LTD.
XX Rubinstein M, Liu B, Novick D, Dinarello C, Graber P;
XX WPI: 2001-006910/01.
XX N-PSDB; AAC62200.
XX Preparation of biologically active molecules from its inactive
XX precursors, comprises mutating their native cleavage site to a site
XX capable of being cleaved by protease and cleaving the mutated molecule
XX .
XX Disclosure; Fig 8a-b; 40pp; English.
XX The present sequence represents a human pro interleukin-18 (IL-18)
XX with a caspase-8 cleavage site. The natural cleavage site of IL-18
XX was mutated to a site susceptible to cleavage by a common protease.
XX The specification describes a method for the preparation of biologically
XX active molecules from their biologically inactive precursors. The method
XX comprises mutating the native cleavage site to a site capable of being
XX cleaved by a protease and cleaving the mutated molecule to yield the
XX active compound. The method is especially used to produce active
XX cytokines, such as IL-18.
XX Sequence 193 AA;

Query Match 100.0%; Score 816; DB 19; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.6e-83;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTIFILSMYKDSQPRGM 60
Db 37 yfgklesklsvirnlndqvlfidqgnrpflfedmtdsdcrdnaprtifilsmyskdsqprgm 96
QY 61 AVTISVKCEKISTLSCENKIISFKENPPDNINKDTKSDIIFFORSVPGHDNKNMQFESSY 120
Db 97 avtisivkcekistlscenkiisfkemppdninkdtsdiiffgrsvpghdnknmqfessy 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 157 egyflacekerdflklllkkedelgdrsimftvqned 193

RESULT 10
AAB30541
ID AAB30541 standard; Protein; 193 AA.
XX AC
XX AAB30541;
XX 06-MAR-2001 (first entry)
XX A human IL-18 with a caspase-8 cleavage site.
XX Protease cleavage site; caspase-1; interleukin-18; IL-18; protease.
XX Synthetic.
XX Homo sapiens.
XX

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FH Key Location/Qualifiers
FT Cleavage-site 33..36
FT /note= "caspase-8 cleavage site"
XX WO200061768-A2..
XX 19-OCT-2000..
XX 13-APR-2000; 2000WO-IL00220.
XX 13-APR-1999; 99IL-0129427.
XX (YEDA ) YEDA RES & DEV CO LTD.
XX Rubinstein M, Liu B, Novick D, Dinarello C, Graber P;
XX WPI: 2001-006910/01.
XX N-PSDB; AAC62200.
XX Preparation of biologically active molecules from its inactive
XX precursors, comprises mutating their native cleavage site to a site
XX capable of being cleaved by protease and cleaving the mutated molecule
XX .
XX Disclosure; Fig 8a-b; 40pp; English.
XX The present sequence represents a human pro interleukin-18 (IL-18)
XX with a caspase-8 cleavage site. The natural cleavage site of IL-18
XX was mutated to a site susceptible to cleavage by a common protease.
XX The specification describes a method for the preparation of biologically
XX active molecules from their biologically inactive precursors. The method
XX comprises mutating the native cleavage site to a site capable of being
XX cleaved by a protease and cleaving the mutated molecule to yield the
XX active compound. The method is especially used to produce active
XX cytokines, such as IL-18.
XX Sequence 193 AA;

Query Match 100.0%; Score 816; DB 22; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.6e-83;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTIFILSMYKDSQPRGM 60
Db 37 yfgklesklsvirnlndqvlfidqgnrpflfedmtdsdcrdnaprtifilsmyskdsqprgm 96
QY 61 AVTISVKCEKISTLSCENKIISFKENPPDNINKDTKSDIIFFORSVPGHDNKNMQFESSY 120
Db 97 avtisivkcekistlscenkiisfkemppdninkdtsdiiffgrsvpghdnknmqfessy 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 157 egyflacekerdflklllkkedelgdrsimftvqned 193

RESULT 11
AAG63830
ID AAG63830 standard; Protein; 193 AA.
XX AC
XX AAG63830;
XX 26-NOV-2001 (first entry)
XX Amino acid sequence of human interleukin 18 (IL-18).
XX T-cell-helper type 2 response; Th2 response; T cell mediated response;
XX allergic response; interleukin 18; IL-18; IGE-mediated allergy;
XX allergic asthma; anaphylactic reaction; asthma associated allergy;
XX IGE dependent allergic rhinoconjunctivitis.
XX Homo sapiens.
XX

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PN W0200168896-A1.
XX
PD 20-SEP-2001.
XX
PF 02-MAR-2001; 2001WO-US06869.
XX
PR 10-MAR-2000; 2000US-0188311.
XX
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI Levy S, Dekruyff RH, Umetsu DT, Maecker H;
XX WPI; 2001-570874/64.
XX DR N-PSDB; AAH78060.
XX
PT Reducing antigen specific immune response in conditions such as asthma,
PT allergic rhinitis, by reducing a T-cell-helper type 2 T cell mediated
PT antigen-specific allergic response .
XX
PS Disclosure; Page 36; 38pp; English.
XX
CC The specification describes a method for reducing a T-cell-helper
CC type 2 (Th2) T cell mediated antigen-specific allergic response. The
CC method comprises administering a DNA construct encoding a fusion
CC protein of interleukin 18 (IL-18) and an antigen associated with the
CC allergic response. The method is useful for reducing a Th2 T cell
CC mediated antigen-specific allergic response especially IgE-mediated
CC allergic asthma or anaphylactic reactions or IgE dependent allergic
CC rhinoconjunctivitis, and for treating asthma associated allergies where
CC the allergies are ongoing at the time of the administration. The
CC present sequence represents a human IL-18, and is used to construct
CC fusion proteins of the invention.
XX
SQ Sequence 193 AA;

Query Match 100.0%; Score 816; DB 22; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.6e-83;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
DB 37 YGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 96
QY 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNKDKTSDIFFQRSVPGHDNKMQFESSY 120
DB 97 AVTISVKCEKISTLSCENKIISFKEMNPPDNKDKTSDIFFQRSVPGHDNKMQFESSY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193

RESULT 12
AAW77082
ID AAW77082 standard; Protein; 193 AA.
XX
AC AAW77082;
XX
DT 16-NOV-1998 (first entry)
XX
DE Interleukin 18 active protein and precursor.
XX
KW Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
KW osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
KW chronic rheumatoid arthritis; deformity otitis; primary hyperthyroidism.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..36
FT Peptide /note= "Signal peptide"
FT Peptide 37..193

/note= "Mature peptide"

FT XX EP861663-A2.
PN XX
PD 02-SEP-1998.
XX
PF 24-FEB-1998; 98EP-0301352.
XX
PR 25-FEB-1997; 97JP-0055468.
XX
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;
XX WPI; 1998-448964/39.
XX DR N-PSDB; V4828.
XX
PT Use of interleukin-18 to inhibit osteoclast formation - in treatment
PT of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
PT osteosarcoma, chronic rheumatoid arthritis, deformity otitis,
PT primary hyperthyroidism and osteoporosis
XX
PS Disclosure; Page 24-28; 56pp; English.
XX
CC Interleukin-18 (IL-18) or a functional equivalent can be used for
CC inhibition of osteoclast formation. IL-18 is used for treating or
CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
CC arthritis, deformity otitis, primary hyperthyroidism, osteopenia and
CC osteoporosis.
XX
SQ Sequence 193 AA;

Query Match 99.6%; Score 813; DB 19; Length 193;
Best Local Similarity 99.4%; Pred. No. 3.5e-83;
Matches 156; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
DB 37 YGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 96
QY 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNKDKTSDIFFQRSVPGHDNKMQFESSY 120
DB 97 AVTISVKCEKISTLSCENKIISFKEMNPPDNKDKTSDIFFQRSVPGHDNKMQFESSY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193

RESULT 13
AAR99564
ID AAR99564 standard; Protein; 157 AA.
XX
AC AAR99564;
XX
DT 29-SEP-1996 (first entry)
XX
DE Human interferon-gamma inducer protein.
XX
KW Interferon-gamma inducer protein; IFN-gamma; antiviral; virucide;
KW antitumour; antibacterial; immunoregulator; adoptive immunotherapy;
KW therapy; cancer.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 73
FT /label= Ile, Thr
PN EP712931-A2.
XX
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PD XX 22-MAY-1996.
XX PN
XX PF
XX PD
XX 10-NOV-1995; 95EP-0308055.
XX XX
XX 29-SEP-1995; 95JP-0274988.
XX PR 15-NOV-1994; 94JP-0304203.
XX PR 23-FEB-1995; 95JP-0058240.
XX PR 10-MAR-1995; 95JP-0078357.
XX PR 18-SEP-1995; 95JP-0262062.
XX XX
XX PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX XX
XX PI Fukuda S, Kohno K, Kunikata T, Kurimoto M, Okamura H;
XX PI Taniguchi M, Tanimoto T, Torigoe K, Ushio S;
XX DR WPI; 1996-252837/26.
XX DR N-PSDB; AAT32411.
XX XX
XX DNA encoding interferon-gamma prodn.-inducing polypeptide - useful
PT to treat and prevent, e.g. viral disease, malignancies and immune
PT disorders
XX XX
XX Example B-1-1; Page 28; 48pp; English.
XX XX
XX A novel human protein (AAR99564) that induces interferon-gamma
CC (IFN-gamma) prodn. by immunocompetent cells is the product of a
CC phage cDNA clone (AAT32411) derived from a human liver library.
CC PCR amplification of the cDNA (see also AAT32409-10) and expression
CC in Escherichia coli Xl-1 Blue MRF-Kan allowed prodn. of recombinant
CC inducer protein. This was used to construct hybridoma H-1, which
CC produced anti-IFN-gamma inducer protein monoclonal antibody H-1mAb,
CC useful in the detection and purification of the inducer protein
CC (see also AAR99558).
XX XX
XX Sequence 157 AA;

Query Match 99.4%; Score 811; DB 17; Length 157;
Best Local Similarity 99.4%; Pred. No. 4.5e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSCDRNAPRTIFIISMVKDSQPRGM 60
Db 1 yfgklesklsvirnlndqvlfidqgnrplfedmtsdcdndnprtifilismykdsgprgm 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTSDIIFFQFORSVPGHKNKQFESSY 120
Db 61 avtisvkcekislscenkliisfkemppdnikdtsdiiffqforsvpgghnknqfessy 120
QY 121 EGYFLACEKERDLFKLILKKKEDELGDRLSMTFTVQNE 157
Db 121 egyflacekerdlfkilkkkedelgdrslmftvqned 157

RESULT 14
AAR99558
ID AAR99558 standard; Protein; 157 AA.
XX AC
XX AAR99558;
XX XX
XX 29-SEP-1996 (first entry)
XX DE
XX Human mature interferon-gamma inducer protein.
XX XX
XX Interferon-gamma inducer protein; IFN-gamma; antiviral; virucide;
KW antitumour; antibacterial; immunoregulator; adoptive immunotherapy;
KW therapy; cancer.
XX XX
XX Homo sapiens.
XX OS
XX Key Location/Qualifiers
FH Misc-difference 73 /label= Ile, Thr
FT

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XX EP712931-A2.
XX PN
XX PD
XX 22-MAY-1996.
XX XX
XX 10-NOV-1995; 95EP-0308055.
XX XX
XX 29-SEP-1995; 95JP-0274988.
XX PR 15-NOV-1994; 94JP-0304203.
XX PR 23-FEB-1995; 95JP-0058240.
XX PR 10-MAR-1995; 95JP-0078357.
XX PR 18-SEP-1995; 95JP-0262062.
XX XX
XX PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX XX
XX PI Fukuda S, Kohno K, Kunikata T, Kurimoto M, Okamura H;
XX PI Taniguchi M, Tanimoto T, Torigoe K, Ushio S;
XX DR WPI; 1996-252837/26.
XX DR N-PSDB; AAT32402.
XX XX
XX DNA encoding interferon-gamma prodn.-inducing polypeptide - useful
PT to treat and prevent, e.g. viral disease, malignancies and immune
PT disorders
XX XX
XX Claim 1; Page 40; 48pp; English.
XX XX
XX A novel human protein (AAR99558) induces interferon-gamma (IFN-gamma)
CC prodn. by immunocompetent cells. It enhances the cytotoxicity of
CC killer cells and/or induces the formation of killer cells (e.g.
CC NK cells, lymphokine-activating killer (LAK) cells, and cytotoxic
CC T-cells). Recombinant IFN-gamma inducer protein can be produced in
CC high yields using host cells, esp. Escherichia coli, transformed
CC with a vector carrying the encoding cDNA (AAT32402). It is useful
CC as an antiviral, antitumor, antibacterial, immunoregulatory and
CC blood platelet enhancing agent, and can be used in adoptive
CC immunotherapy. It is also used to raise monoclonal antibodies.
XX A full-length sequence is given in AAR99560.
XX XX
XX Sequence 157 AA;

Query Match 99.4%; Score 811; DB 17; Length 157;
Best Local Similarity 99.4%; Pred. No. 4.5e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSCDRNAPRTIFIISMVKDSQPRGM 60
Db 1 yfgklesklsvirnlndqvlfidqgnrplfedmtsdcdndnprtifilismykdsgprgm 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTSDIIFFQFORSVPGHKNKQFESSY 120
Db 61 avtisvkcekislscenkliisfkemppdnikdtsdiiffqforsvpgghnknqfessy 120
QY 121 EGYFLACEKERDLFKLILKKKEDELGDRLSMTFTVQNE 157
Db 121 egyflacekerdlfkilkkkedelgdrslmftvqned 157

RESULT 15
AAW15701
ID AAW15701 standard; protein; 157 AA.
XX AC
XX AAW15701;
XX XX
XX 26-JAN-1998 (first entry)
XX DE
XX Interferon-gamma inducer protein.
XX XX
XX Interferon-gamma, IFN-gamma; antiviral; antioncotic; radiotherapy;
KW immunoregulatory; antitumour agent; chemotherapy; leukopaenia;
KW thrombocytopaenia; immunocompetent cell; asthma; hayfever;
KW rheumatism; interleukin; killer cell.

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XX	Homo sapiens.	
XX	OS	
XX	Key	Location/Qualifiers
FT	Misc-difference 73	
FT	FT	/label= Ile, Thr
XX		
PN	EP767178-A1.	
XX	09-APR-1997.	
XX	26-SEP-1996;	96EP-0306997.
XX	20-SEP-1996;	96JP-0269105.
XX	26-SEP-1995;	95JP-0270725.
PR	29-FEB-1996;	96JP-0067434.
XX		
XX	(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.	
PA		
XX	Akita K, Fujii M, Kurimoto M, Nukada Y, Tanimoto T;	
PI		
XX	WPI; 1997-205381/19.	
DR		
XX		
PT	Human protein that induces interferon-gamma prodn. in	
PT	immuno:competent cells - useful for adoptive immuno:therapy of	
PT	tumours and as antimicrobial agent etc.	
XX		
PS	Claim 8; Page 20; 26pp; English.	
XX		
CC	The present sequence represents a novel protein from human cells, which	
CC	induces interferon-gamma (IFN gamma) production in immunocompetent cells.	
CC	This protein enhances cytotoxicity of killer cells and induces their	
CC	formation. It is used as an antioncotic agent for antitumour	
CC	immunotherapy, an antiviral (including anti-AIDS) or antibacterial agent,	
CC	and in the treatment of atopic or immune system diseases, e.g. asthma,	
CC	hayfever or rheumatism. When formulated with interleukin-3, it is also	
CC	used to treat leukopaenia and thrombocytopaenia associated with	
CC	radiotherapy or chemotherapy of leukaemia and other cancers. When used in	
CC	antitumour immunotherapy, this novel protein significantly improves the	
CC	immunotherapeutic effect of interleukin-2 (IL-2) compared with use of	
CC	IL-2 alone, either when administered to the patient (before	
CC	administration of IL-2) or by addition to the medium in which cells	
CC	(intended for return to the patient) are being grown.	
XX		
SQ	Sequence 157 AA;	

Query Match	99.4%	Score 811;	DB 18;	Length 157;
Best Local Similarity	99.4%;	Pred. No. 4.5e-83;		
Matches 156;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy 1	YFGLESKLSVIRNLNQVLFIDQGNPLFEDMTDSOCRDNAPTIFIIISMYKDSQPRGM 60			
Db 1	yfglesklsvirnlndqvlfidggnrplfmedtdsdcdrdnaptifilismykdspqrgm 60			
Qy 61	AVTISVACEKISTLSCENKIISPRKEMPPDNIKTKSDIIFQFSVPGHDKNMQFESSY 120			
Db 61	avtislvtckelislscenkiisfremppdniktkdsdliifqgrsvphdknmqfessy 120			
Qy 121	EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157			
Db 121	egyflacekerdlfklllkkedelqdrsimftvqned 157			

Search completed: October 8, 2002, 10:15:15
Job time: 276 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 8, 2002, 10:15:51 ; Search time 28.21 seconds
(without alignments)
534.776 Million cell updates/sec

Title: SEQ6THRAT73

Perfect score: 816

Sequence: 1 YFKLESKLSVIRNLNDQVL.....LKKDELGRSIMFTVQNED 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_71.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	520	63.7	192	2 S60226	cytokine IGIF - mouse
2	85	10.4	381	2 T40341	hypothetical prote
3	81.5	10.0	270	1 S10532	interleukin-1 alph
4	81	9.9	263	2 T39487	hypothetical prote
5	80.5	9.9	866	2 C71509	probable DNA polym
6	80.5	9.9	1663	1 C3MS	complement C3 prec
7	80	9.8	2470	2 I50726	cation-independent
8	79	9.7	452	2 D64583	hypothetical prote
9	79	9.7	680	2 A28121	major merozoite su
10	79	9.7	1772	2 A45532	hypothetical prote
11	78.5	9.6	204	2 T44357	hypothetical prote
12	78	9.6	473	2 T32038	hypothetical prote
13	77.5	9.5	1251	2 A56677	neuronal cell cycl
14	77	9.4	364	2 A81261	probable periplasm
15	76.5	9.4	425	2 T25457	hypothetical prote
16	76	9.3	632	2 T00679	hypothetical prote
17	76	9.3	747	2 E84698	hypothetical prote
18	75.5	9.3	192	2 S15661	(3'-5')oligo(A) sy
19	75.5	9.3	270	2 T46620	interleukin-1 alph
20	75.5	9.3	467	2 A48713	serine/threonine-s
21	75.5	9.3	578	2 H82872	hypothetical prote
22	75	9.2	467	2 T49609	proto-oncogene pro
23	74.5	9.2	1064	1 S57450	protein-tyrosine k
24	74.5	9.1	334	2 T04198	hypothetical prote
25	74.5	9.1	351	2 E71372	probable translati
26	74.5	9.1	1036	2 H64245	hypothetical prote
27	74.5	9.1	1228	2 A57384	multimerin, endoth
28	74.5	9.1	1510	2 T16927	hypothetical prote
29	74	9.1	245	2 B90488	hypothetical prote

30	74	9.1	361	2 E96904	minD family ATPase
31	74	9.1	376	2 T24925	hypothetical prote
32	74	9.1	467	2 A47388	serine/threonine p
33	74	9.1	810	2 B71639	virb4 protein prec
34	74	9.1	2663	1 S28261	centromere protein
35	73.5	9.0	268	2 H85641	probable small sub
36	73.5	9.0	268	2 C90781	probable small sub
37	73.5	9.0	389	2 B69277	TRK potassium upa
38	73.5	9.0	432	2 C90268	conserved hypothet
39	73.5	9.0	475	2 T32036	hypothetical prote
40	73.5	9.0	888	2 A38539	p101 protein precu
41	73.5	9.0	1997	2 F71607	DNA helicase II BR
42	73	8.9	418	2 D82932	seryl-trNA synthet
43	73	8.9	447	2 T26293	hypothetical prote
44	72.5	8.9	268	1 TCB01A	interleukin-1 alph
45	72.5	8.9	268	1 B24073	interleukin-1 alph

ALIGNMENTS

RESULT 1

S60226

cytokine IGIF - mouse

C:Species: Mus musculus (house mouse)

C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000

C:Accession: S60226

R:Okamura, H.; Tsutsui, H.; Komatsu, T.; Yutsudo, M.; Hakura, A.; Tanimoto, T.; Tori

Nature 378, 88-91, 1995

A:Title: Cloning of a new cytokine that induces IFN-gamma production by T cells.

A:Reference number: S60226; MUID:96061009

A:Accession: S60226

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-192 <OKA>

A:Cross-references: EMBL:D49949; NID:g1064822; PIDN:BAA08705.1; PID:g1064823

C:Superfamily: Mus musculus cytokine IGIF

Query Match 63.7%; Score 520; DB 2; Length 192;

Best Local Similarity 65.6%; Pred. No. 1.2e-41;

Matches 101; Conservative 27; Mismatches 24; Indels 2; Gaps 2;

Qy 2 FGLKLESKLSVIRNLNDQVLFDQGNRPLFEDMTSDCRONAPRTIFILSMYKDSQPRGMA 61

Db 37 FGLRHCTTAVIRNLNDQVLFDVK-RQPVFEDMTDIDQSAEPQTRLIILYMYKDSVIRGLA 95

Qy 62 VTISVKCEKISLSCENKIIISFKEMNPPDNITKDTSDIIFQSRVPGHDKMKQFESSSYE 121

Db 96 VTLVKDKSKMTSLCKNKIIISFEEMDPDENIDDDIQSDLIFFQKRVPGH-NKMEFESSLYE 154

Qy 122 GYFLACERDLFKLILKKEDELGRSIMFTVQN 155

Db 155 GHFLACQKDEDAFKLILKKEDEKDKSVMTLTN 188

RESULT 2

T40341

hypothetical protein SPBC3B9.02c - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T40341

R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z21922

A:Accession: T40341

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-381 <WOO>

A:Cross-references: EMBL:AL022070; PIDN:CAAL17782.1; GSPDB:GN00067; SPDB:SPBC3B9.02c

A:Experimental source: strain 972h-; cosmid c3B9

C:Genetics:


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Db      217 EQYKELLPGK--VTVSTPAVAVTTLAADAPATPEGAVPGAVPGAVPGAV--PGAV 272
        ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy      107 PGHDNKKQFESSYEGYFLACERDLFKLILKKEDELGRSINFVTFQNE 156
        ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      273 PGGSDTRFVAGSSVDD-----NEDDDIIQIATSGQSEDAPEKDILSEFTNE 317
        ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 10
A45532
major merozoite surface antigen precursor - Plasmodium yoelii1
C:Species: Plasmodium yoelii1
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 26-Aug-1999
C:Accession: A45532; A45531
R:Lewis, A.P.
Mol. Biochem. Parasitol. 36, 271-282, 1989
A:Title: Cloning and analysis of the gene encoding the 230-kilodalton merozoite surface antigen
A:Reference number: A45532; MUID:90014981
A:Accession: A45532
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1772 <LEW>
A:Cross-references: GB:J04668; NID:g160492; PID:g160493
R:Daly, T.M.; Burns Jr., J.M.; Long, C.A.
Mol. Biochem. Parasitol. 36, 283-285, 1989
A:Title: Precursor to the major merozoite surface antigen of Plasmodium yoelii1: clone 1
A:Reference number: A45531; MUID:90014982
A:Accession: A45531
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 454-1094 <DAL>
A:Cross-references: GB:J03975; NID:g160081; PID:g160082
C:Superfamily: major merozoite surface antigen
C:Keywords: surface antigen

Query Match          9.7%; Score 79; DB 2; Length 1772;
Best Local Similarity 19.4%; Pred. No. 52;
Matches 33; Conservative 36; Mismatches 75; Indels 26; Gaps 7;

Qy      2 FGKLESKLIVRLNL---DQVLFDIGNRLPFE-----DMTDSDCRDNPRTIFII 49
        ::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      1251 YSRLEELRK--KNINLGKERISVGGHLHVEEFEEKLIKDKOYTGKKNDPNAPEVTNAF 1308
        ::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Qy      50 SMYKDSOPRGMAVTISKYCEKISLSCENKIISFKEMNP---PDNIKDTKSDIIFFORSV 106
        ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      1309 EQYKELLPGK--VTVSTPAVAVTTLAADAPATPEGAVPGAVPGAVPGAV--PGAV 1364
        ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Qy      107 PGHDNKKQFESSYEGYFLACERDLFKLILKKEDELGRSINFVTFQNE 156
        ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      1365 PGGSDTRFVAGSSVDD-----NEDDDIIQIATSGQSEDAPEKDILSEFTNE 1409
        ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 11
T44357
hypothetical protein [imported] - Clostridium histolyticum
C:Species: Clostridium histolyticum
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T44357
R:Watsushita, O.; Jung, C.M.; Katayama, S.; Minami, J.; Takahashi, Y.; Okabe, A.
J. Bacteriol. 181, 923-933, 1999
A:Title: Gene duplication and multiplicity of collagenases in Clostridium histolyticum
A:Reference number: Z22752; MUID:99121032
A:Accession: T44357
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-204 <WAT>
A:Cross-references: EMBL:AB014075; NID:g3868863; PIDN:BAA34544.1; PID:g3892648
A:Experimental source: strain JCM 1403

Query Match          9.6%; Score 78.5; DB 2; Length 204;
Best Local Similarity 26.4%; Pred. No. 4.5;

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Query Match          9.5%; Score 77.5; DB 2; Length 1251;
Best Local Similarity 23.5%; Pred. No. 48;
Matches 38; Conservative 37; Mismatches 64; Indels 23; Gaps
9:

QY 6 ESKLSVI-RNLNDQVLFI---DQGNRLPFDWMTSDSCRDNAPRIFIISMVKYDQSPRGM 61
   ||| : : ||| : : ||| : : ||| : : ||| : : ||| : : ||| : :
Db 648 EEKLAQIQKEMEDQEVITQGYQQENRKYKOMKDLQIQNKKNES---OMYKENOCL-MS 702
   ||| : : ||| : : ||| : : ||| : : ||| : : ||| : : ||| : :

QY 62 VTISVKEKISTLSCENKIITSFKEMNPNPDNIKDTKSDIIFQSRVPGHDNKKQFE---- 116
   ||| : : ||| : : ||| : : ||| : : ||| : : ||| : : ||| : :

```

```

Qy 117 -SSSYGCGYFLACBKRDLFKLLKKEDELGDRSIMFTVQNE 156
      :      :||||| 1 :      :||| :
Db 758 QDKOALELDLQGAKKERDLAKVQITSTS--SEKSYEFKIMEE 797

RESULT 14
A81261
probable periplasmic protein Cjl643 [imported] - Campylobacter jejuni (strain NCTC 11163)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
C:Accession: A81261
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chli
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Ba
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals
A:Reference number: A81250; MUID:20150912
A:Accession: A81261
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-364 <FAR>
A:Cross-references: GB:AL139079; GB:AL111168; MID:96968971; PIDN:CAB73631.1; PID:9696
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: Cjl643

```

Query Match	9.4%	Score 77	DB 2	Length 364
Best Local Similarity	24.8%	Pred. No. 12		
Matches 38	Conservative 21	Mismatches 40	Indels 54	Gaps
Qy	12	IRNLNDQVLFIDCGNRPLFEEDMTDSDCRD--NAPRTIFIIISWYK-----DSOPR-----	58	
Db	211	LRKLNKILFADRGSTLYFQVLRDN--MDLNISTEVFAKDLSPFNLPDskPKPKITNFTS	268	
Qy	59	--GMAVTSYKCEKI-----STLSCENKII--SEKEMPPNNI-----	92	
Db	269	NLGLTVNASLVVTKIDPKSKVSNAGVGDKILRVNIIILNFKEL--QNILSAGNDFS	322	
Qy	93	-----KTKSDIIIFQSRVPGH-----DNKMQF	115	
Db	326	ILIERKSTKPLPSNFNNELGGSNANSGGDKGFQF	358	

```

RESULT 15
T25457
hypothetical protein B0432.9 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text
C:Accession: T25457
R:Henkhaus, J.; Wohldmann, P.
submitted to the EMBL Data Library, December 1996
A:Description: the sequence of C. elegans cosmid B0432.
A:Reference number: Z20038
A:Accession: T25457
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-425 <EN>
A:Cross-references: EMBL:U08036; PIDN:AAB37893.1; GSPDB:

```

A;Residues: 1-423 (HEN)
A;Cross-references: EMBL:U80836; PIDN:AAB37893.1; GSPDB:GN00020: CESP:B0432.9

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 8, 2002, 10:17:03 ; Search time 15.78 Seconds
(without alignments)
385.233 Million cell updates/sec

Title: SEQ6THRAT73

Perfect score: 816

Sequence: 1 YFGKLESKSLVIRNLNDQVL.....LKKEDELGDRSIMFTVQNE 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	816	100.0	193	IL18_HUMAN	Q14116 homo sapien
2	664	81.4	193	IL18_HORSE	Q9XSQ7 equus caball
3	659	80.8	193	IL18_BOVIN	Q9TU73 bos taurus
4	642	78.7	192	IL18_PIG	O19073 sus scrofa
5	618	75.7	193	IL18_CANFA	Q9XSR0 canis famil
6	520	63.7	192	IL18_MOUSE	P70380 mus musculus
7	519.5	63.7	194	IL18_RAT	P97636 rattus norv
8	81.5	10.0	270	IL1A_PIG	P18430 sus scrofa
9	81	9.9	267	IL1A_RABIT	P04822 oryctolagus
10	80.5	9.9	1663	CO3_MOUSE	P01027 mus musculus
11	79	9.7	1772	MSPI_PLAYO	P13828 plasmodium
12	77.5	9.5	270	IL1A_HORSE	Q28385 equus caball
13	75.5	9.3	192	OSAB_MOUSE	Q60856 mus musculus
14	75	9.2	467	M3K8_MOUSE	Q07174 mus musculus
15	74.5	9.1	351	RF1_TREPA	O83090 treponema p
16	74.5	9.1	1036	Y414_MYCGE	P47653 mycoplasma
17	74.5	9.1	1228	ECM_HUMAN	Q13201 homo sapien
18	74	9.1	270	IL1A_FELCA	O46613 felis silve
19	74	9.1	467	M3K8_RAT	Q63562 rattus norv
20	74	9.1	2663	CENE_HUMAN	Q02224 homo sapien
21	73	8.9	4590	FATH_HUMAN	Q14517 homo sapien
22	72.5	8.9	268	IL1A_BOVIN	P08831 bos taurus
23	72.5	8.9	313	COLA_ARATH	Q9M9B3 arabidopsis
24	72.5	8.9	467	M3K8_HUMAN	P11279 homo sapien
25	72	8.8	426	YXCX_ASTILO	P81551 astasia ion
26	72	8.8	700	NONA_DROME	Q04047 drosophila
27	72	8.8	800	K1N4_YEAST	Q01919 saccharomyc
28	71.5	8.8	268	IL1A_CAPHI	P79161 capra hircu
29	71.5	8.8	375	YVC5_CAEEL	Q18610 caenorhabdi
30	71.5	8.8	377	NGK1_HUMAN	P16333 homo sapien
31	71.5	8.8	527	RAG2_HUMAN	P55895 homo sapien
32	71	8.7	198	V511_ROTNA	P17467 rabbit rota
33	70.5	8.6	268	IL1A_SHEEP	Q28579 ovis aries

34	70.5	8.6	642	1	FLID_CAMJE	O9phw6 campylobact
35	70.5	8.6	704	1	YGZ9_YEAST	P53061 saccharomyc
36	70.5	8.6	1091	1	ITA6_MOUSE	O61739 mus musculus
37	70.5	8.6	1230	1	SMC3_YEAST	P47037 saccharomyc
38	70	8.6	451	1	VPS9_YEAST	P25787 saccharomyc
39	70	8.6	1486	1	MUKB_ECOLI	P22523 escherichia
40	70	8.6	1647	1	SN24_HUMAN	P51532 homo sapien
41	69.5	8.5	582	1	CRTI_CAPAN	P80093 capsicum an
42	69.5	8.5	644	1	YGM4_YEAST	P53129 saccharomyc
43	69.5	8.5	919	1	RFO2_CAPVK	P16716 capripoxvir
44	69	8.5	492	1	UBID_PASMR	Q9cp43 pasteurella
45	69	8.5	578	1	TRM1_DROME	Q9vkh9 drosophila

ALIGNMENTS

```

RESULT 1
IL18_HUMAN
ID IL18_HUMAN STANDARD; PRT; 193 AA.
AC Q14116; O75599;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
CN IL18 OR IGIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96247646; PubMed=8666798;
RA Ushio S., Namba M., Okura T., Hattori K., Nukada Y., Akita K.,
RA Tanabe F., Konishi K., Micallef M., Fujii M., Torigoe K., Tanimoto T.,
RA Fukuda S., Ikeda M., Okamura H., Kurimoto M.;
RT "Cloning of the cDNA for human IFN-gamma-inducing factor, expression
RT in Escherichia coli, and studies on the biologic activities of the
RT protein.";
RL J. Immunol. 156:4274-4279(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Yong D., Guixin D., Lihua H., Haitao W.;
RT "Cloning and sequencing of the cDNA for precursor hIL-18.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Liu J., Peng X., Yuan J., Qiang B.;
RT "Cloning of human Interleukin 18 cDNA.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 2-193 FROM N.A.
RC TISSUE=Peripheal blood;
RA Conti B., Kim S.J., Tinti C., Chun H.S., Joh T.H.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
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CC -----
CC EMBL; D49950; BAA08706.1; -.
CC EMBL; AF077611; AAC37787.1; -.

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DR EMBL; AY04641; AAK95950.1; -.
DR EMBL; U90434; AAB50010.1; -.
DR MIM; 600953; -.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
FT CONFLICT 66 66 F -> L (IN REF. 2).
FT CONFLICT 86 86 S -> R (IN REF. 2).
FT CONFLICT 191 191 N -> S (IN REF. 2).
SQ SEQUENCE 193 AA; 22326 MW; 323C62C203788D55 CRC64;

Query Match 100.0%; Score 816; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.6e-68;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTFIISMVKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTFIISMVKDSQPRGM 96

QY 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIDKTSDIFFORSVPGHDKNKQFESSY 120
DB 97 AVTISVKCEKISTLSCENKIISFKEMNPPDNIDKTSDIFFORSVPGHDKNKQFESSY 156

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193

RESULT 2
IL18_HORSE
ID IL18_HORSE STANDARD; PRT; 193 AA.
AC QXQSQT;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Interleukin-18 precursor (IL-18) (Interleukin-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Nicolson L., Penha-Goncalves M.N., Keanie J.L., Logan N.A.,
RA Argyle D.J., Onions D.E.;
RT "Nucleotide sequence of equine interleukin 12 and 18 cDNAs.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
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CC -----
DR EMBL; Y1131; CAAY2013.1; -.
DR Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
SQ SEQUENCE 193 AA; 22058 MW; 4D81535E9004ECAF CRC64;

Query Match 81.4%; Score 664; DB 1; Length 193;
```

```
Best Local Similarity 78.3%; Pred. No. 1.7e-54;
Matches 123; Conservative 21; Mismatches 13; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTFIISMVKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTFIISMVKDSQPRGM 96

QY 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIDKTSDIFFORSVPGHDKNKQFESSY 120
DB 97 AVTISVKCEKISTLSCENKIISFKEMNPPDNIDKTSDIFFORSVPGHDKNKQFESSY 156

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193

RESULT 3
IL18_BOVIN
ID IL18_BOVIN STANDARD; PRT; 193 AA.
AC Q9TU73;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interleukin-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20012648; PubMed=10547157;
RA Shoda L.K., Zarlenga D.S., Hirano A., Brown W.C.;
RT "Cloning of a cDNA encoding bovine interleukin-18 and analysis of IL-
RT 18 expression in macrophages and its IFN-gamma-inducing activity.";
RL J. Interferon Cytokine Res. 19:1169-1177(1999).
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
CC -----
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CC -----
DR EMBL; AF124789; AAF08686.1; -.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
SQ SEQUENCE 193 AA; 22347 MW; 65720F199DEA49C4 CRC64;

Query Match 80.8%; Score 659; DB 1; Length 193;
Best Local Similarity 77.7%; Pred. No. 4.9e-54;
Matches 122; Conservative 23; Mismatches 12; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTFIISMVKDSQPRGM 60
DB 37 HFGKLEPKLSIIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTFIISMVKDSQPRGM 96

QY 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIDKTSDIFFORSVPGHDKNKQFESSY 120
DB 97 AVTISVKCKRMSTLSCENKIISFKEMNPPDNIDNEESDIFFORSVPGHDKNKQFESSY 156
```

Qy 121 EGYFLACEKERDLFKLILKKEDELDGDRSIMEFTVQNED 157
:|||||:| | |||||:| :|:|||||::
Dd 157 KGYFLACKKENDLFKLILKKDDNRDKSVMEFTVQNQN 193

```

RESULT 4
IL18_PIG
ID IL18_PIG STANDARD; PRT; 192 AA.
AC Q19073;
DT 15-JUL-1998 (Rel. 36, Created)
DT 13-DEC-1998 (Rel. 37, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
[1]
RN SEQUENCE FROM N.A.
RA Foss D.L., Murtaugh M.P.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RA Muneta Y., Mori Y.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RA Tissue=Intestine;
RC MEDLINE=20260994; PubMed=10803849;
RX Fournout S., Dozolis C.M., Yerle M., Pinton P., Fairbrother J.M.,
RA Oswald E., Oswald I.P.;
RT "Cloning, chromosomal location, and tissue expression of the gene for
RT p19 Interleukin-18.";
RC Immunogenetics 51:358-365(2000).
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
-----
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-----
DR EMBL; U68701; AAC18415.1; -
DR EMBL; AB010003; BAA24135.1; -
DR EMBL; AF191088; AAF71200.1; -
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
DR Cytokine.
FT PROPEP 1 35 BY SIMILARITY.
FT CHAIN 36 192 INTERLEUKIN-18.
SQ SEQUENCE 192 AA; 220206 MW; 881EA654E221A17A CRC64;

```

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Qy 121 EGYFLACEKERDPLKILKKEDELGDRSIMFTVQNE 157
      :|||||:| | | | | | | | | | | | | | | | |
Db 156 KGYFLACKENDPLKILKKECDGKRSIMFTVQKN 192

RESULT 5
IL18_CANFA
ID IL18_CANFA STANDARD; PRT; 193 AA.
AC Q9XSRO;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Canis familiaris (Dog).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OC NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Argyle D.J., McGillivray C., Nicolson L., Onions D.E.;
RT "Cloning, sequencing and characterization of canine interleukin-18.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
-----
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-----
CC EMBL; Y11133; CAA72015.1; -.
DR
KW Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
SQ SEQUENCE 193 AA; 22037 MW; 0D973E586FA61E25 CRC64;

```

```

Query Match      75.7%; Score 618; DB 1; Length 193;
Best Local Similarity 74.4%; Pred. No. 3e-50;
Matches 116; Conservative 23; Mismatches 17; Indels 0; Gaps 0

Qy 1 YFGKLESKLSVIRNLNQVLFIIDQGNRPLEDWTDSCRONAPRTIFIISMYKDSQPRGM 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 37 YFGKLEPKLSIRNLNQVLFLVNEGNOVPFEDMDPSDCTONAPHTIFIIMYKDSLTRL 96
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 AVTISVACEKISTLSCENKIISPKEMPPDNIKTKSDIIFFQRSVPCHDNKMQFESSY 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 97 AVTISVAKYMTLUSCKNKTISFGMKPPDSINDEGNDIIFFQKRSVPCHDDKIOFESSLY 156
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 121 EGYFLACEKERDLEKLIILKKEDELGRSIMFTVQNE 156
    :|||:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 157 KGHEFLACKKENDLEKLIILKOKDENGDKSIMFTVQNK 192
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 6
IL18_MOUSE
ID IL18_MOUSE STANDARD; PRT; 192 AA.
AC P70380;
DT 15-JUL-1998 (Rel. 36, Created)
DR 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Mus musculus (Mouse).

```

[illegible]

```

OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=96061009; PubMed=7477296;
RA Okamura H., Tsutui H., Komatsu T., Yutsudo M., Hakura A.,
RA Tanimoto T., Torigoe K., Okura T., Nukada Y., Hattori K.,
RA Akita K., Namba M., Tanabe F., Konishi K., Fukuda S., Kurimoto M.;
RT "Cloning of a new cytokine that induces IFN-gamma production by T
RT cells.";
RL Nature 378:88-91(1995).
RN [2]
RP SEQUENCE OF 1-191 FROM N.A.
RC STRAIN=NOD; TISSUE=Pancreas;
RX MEDLINE=97174346; PubMed=9022080;
RA Roche H., Jenkins N.A., Copeland N.G., Kolb H.;
RT "Active stage of autoimmune diabetes is associated with the
RT expression of a novel cytokine, IGIF, which is located near Idd2.";
RL J. Clin. Invest. 99:469-474(1997).
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE 1
CC CELLS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
CC -----
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CC -----
DR EMBL; D49949; BAA08705.1; -.
DR EMBL; U66244; AAB49753.1; -.
DR MGD; MGI:107936; IL18.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 35
FT CHAIN 36 192
FT CHAIN 183 185
FT CONFLICT 183 185 MFT -> IS (IN REF. 2).
FT SEQUENCE 192 AA; 22135 MW; 8FED938473874D63 CRC64;
SQ
Query Match 63.7%; Score 520; DB 1; Length 192;
Best Local Similarity 65.6%; Pred. No. 3.3e-41;
Matches 101; Conservative 27; Mismatches 24; Indels 2; Gaps 2;
QY 2 FGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDNAPRTIFIIISMYKDSQPRGMA 61
Db |||:| :||||:|||||:| :|:||||| :|:| :|:| :|:|:|:|:|
37 FGRUHCCTAVIRNLNDQVLFVDK-RQPVFEDMTDIDQASPEQTRLIITYMKDSEVRGLA 95
QY |||:| :||||:|||||:| :|:||||| :|:| :|:| :|:|:|:|:|
62 VTISVCKEISTLSCENKIISFKEMNPPDNKDKSDIIFQFQSVPGHDKNMQFESSY 121
Db |||:| :||||:|||||:| :|:||||| :|:| :|:| :|:|:|:|:|
96 VTLSVKDSKMSLTSCNKNKIISFEEMDPENIDDIQSDLIFFQKRVPGH-NKMEFESSLYE 154
QY 122 GYFLACEKERDLFKLILKKEDELGDRSIMFTVQN 155
Db |||:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
155 GHFLACQKEDDAFKLILKKEDELGDRSIMFTVQN 188
Db |||:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
RESULT 7
IL18_RAT STANDARD; PRT; 194 AA.
AC P97636; P97637; O88749;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)

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```

DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Adrenal gland;
RX MEDLINE=97152963; PubMed=8999896;
RA Conti B., Jahng J.W., Tinti C., Son J.H., Joh T.H.;
RT "Induction of interferon-gamma inducing factor in the adrenal
RT cortex.";
RL J. Biol. Chem. 272:2035-2037(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RX MEDLINE=98368130; PubMed=9702748;
RA Culhane A.C., Hall M.D., Rothwell N.J., Luheshi G.N.;
RT "Cloning of rat brain interleukin-18 cDNA.";
RL Mol. Psych. 3:362-366(1998).
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE 1
CC CELLS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
CC -----
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CC -----
DR EMBL; U77776; AAC53009.1; -.
DR EMBL; U77777; AAC53010.1; -.
DR EMBL; AJ222813; CAA11001.1; -.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
KW Cytokine; Alternative splicing.
FT PROPEP 1 36
FT CHAIN 37 194
FT CHAIN 121 139 MISSING (IN ISOFORM ALPHA).
FT VARSPLIC 121 139 MS -> IP (IN REF. 2).
FT CONFLICT 4 5
FT CONFLICT 48 48 I -> M (IN REF. 2).
FT SEQUENCE 194 AA; 22303 MW; E2089AD6F1798450 CRC64;
SQ
Query Match 63.7%; Score 519.5; DB 1; Length 194;
Best Local Similarity 63.9%; Pred. No. 3.7e-41;
Matches 99; Conservative 28; Mismatches 27; Indels 1; Gaps 1;
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDNAPRTIFIIISMYKDSQPRGM 60
Db |||:| :||||:|||||:| :|:||||| :|:| :|:| :|:|:|:|:|
37 HFGRUHCCTAVIRINDQVLFVDKRNPEVDFMDIDRTANESQTRLIITYMKDSEVRGL 96
QY 61 AVTISVCKEISTLSCENKIISFKEMNPPDNKDKSDIIFQFQSVPGHDKNMQFESSY 120
Db |||:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
97 AVTUSVKDGRMSTLSCNKNKIISFEEMNPPENIDDIKSDLIFFQKRVPGH-NKMEFESSLY 155
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQN 155
Db |||:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
156 EGHFLACQKEDDAFKLILKKEDELGDRSIMFTVQN 190
Db |||:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
RESULT 8
IL1A_PIG STANDARD; PRT; 270 AA.
AC P18430;
DT 01-NOV-1990 (Rel. 16, Created)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)

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Db 127 LRIKQETFLDALNQSLVIRSDSYQLRAAPLQNLGDAVKFMDGYMTSEDSILPVTLRI 186
 QY 67 -KCEKISLSCENKIISFKEM-NPNDINKDKPKSLDILFEQFORSVPGHDKNKMPSESSYEGYF 124
 Db 187 SQTPLFVSAQNEDEPVLVKEMPTPRIITDSESDILFFWET---QGNKNYFKSAANPOLF 243
 QY 125 LACEKE 130
 Db 244 IATKPE 249
 RESULT 10
 CO3_MOUSE STANDARD; PRT; 1663 AA.
 AC P01027;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1996 (Rel. 33, last sequence update)
 DT 01-NOV-1997 (Rel. 35, last annotation update)
 DE Complement C3 precursor (HSE-MSF) [Contains: C3a anaphylatoxin].
 GN C3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=65038854; PubMed=6208565;
 RA Fey G.H., Lundwall A., Wessel R.A., Tack B.F., de Bruijn M.H.L.,
 RA Domdey H.;
 RA "Nucleotide sequence of complementary DNA and derived amino acid
 RT sequence of murine complement protein C3";
 RL Philos. Trans. R. Soc. Lond., B, Biol. Sci. 306:333-344(1984).
 RN [2]
 RP SEQUENCE OF 671-1663 FROM N.A.
 RX MEDLINE=6504819; PubMed=6094532;
 RA Wessel R.A., Lundwall A., Davidson P., Gibson T., Tack B.F., Fey G.H.;
 RA "Structure of murine complement component C3. II. Nucleotide sequence
 RT of cloned complementary DNA coding for the alpha chain";
 RL J. Biol. Chem. 259:13857-13862(1984).
 RN [3]
 RP SEQUENCE OF 671-748 FROM N.A.
 RX MEDLINE=8311730; PubMed=6961437;
 RA Domdey H., Wiebauer K., Kazmaier M., Mueller V., Odink K., Fey G.H.;
 RA "Characterization of the mRNA and cloned cDNA specifying the third
 RT component of mouse complement";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:7619-7623(1982).
 RN [4]
 RP SEQUENCE OF 658-761 FROM N.A.
 RX MEDLINE=84201365; PubMed=6609661;
 RA Fey G.H., Wiebauer K., Domdey H.;
 RA "Amino acid sequences of mouse complement C3 derived from nucleotide
 RT sequences of cloned cDNA";
 RL Ann. N.Y. Acad. Sci. 421:307-312(1983).
 RN [5]
 RP SEQUENCE OF 1-34 FROM N.A.
 RX MEDLINE=83117622; PubMed=6985486;
 RA Wiebauer K., Domdey H., Diggelmann H., Fey G.;
 RA "Isolation and analysis of genomic DNA clones encoding the third
 RT component of mouse complement";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:7077-7081(1982).
 RN [6]
 RP SEQUENCE OF 25-41 AND 749-760.
 RX MEDLINE=93373334; PubMed=8364938;
 RA Hamada J.-I., Cavanaugh P.G., Miki K., Nicolson G.L.;
 RA "A paracrine migration-stimulating factor for metastatic tumor cells
 RT secreted by mouse hepatic sinusoidal endothelial cells:
 RT identification as complement component C3b";
 RL Cancer Res. 53:4418-4423(1993).
 RN [7]
 RP ALTERNATIVE INITIATION
 RX MEDLINE=95053742; PubMed=7964485;
 RA Cahen-Kramer Y., Martenson I.L., Melchers F.;
 RA "The structure of an alternate form of complement C3 that displays

RT costimulatory growth factor activity for B lymphocytes."; J. Exp. Med. 180:2079-2088(1994).
 RL
 CC -1- FUNCTION: C3 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE
 CC COMPLEMENT SYSTEM. ITS PROCESSING BY C3 CONVERTASE IS THE CENTRAL
 CC REACTION IN BOTH CLASSICAL AND ALTERNATIVE COMPLEMENT PATHWAYS.
 CC AFTER ACTIVATION C3B CAN BIND COVALENTLY, VIA ITS REACTIVE
 CC THIOESTER, TO CELL SURFACE CARBOHYDRATES OR IMMUNE AGGREGATES.
 CC -1- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C3,
 CC C3A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
 CC INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
 CC PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
 CC BASOPHILIC LEUCOCYTES.
 CC -1- SUBUNIT: C3 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 ARG
 CC RESIDUES, FORMING TWO CHAINS, BETA & ALPHA, LINKED BY A DISULFIDE
 CC BOND. C3 CONVERTASE ACTIVATES C3 BY CLEAVING THE ALPHA CHAIN,
 CC RELEASING C3A ANAPHYLATOXIN & GENERATING C3B (BETA CHAIN + ALPHA
 CC CHAIN).
 CC -1- ALTERNATIVE PRODUCTS: A SHORT FORM IS PRODUCED BY THE USE OF AN
 CC ALTERNATIVE INITIATION CODON. THIS SHORT CHAIN HAS B-CELL
 CC STIMULATORY ACTIVITY.
 CC -1- MISCELLANEOUS: C3B IS RAPIDLY SPLIT IN TWO POSITIONS BY FACTOR I
 CC AND A COFACTOR TO FORM IC3B (INACTIVATED C3B) AND C3F WHICH IS
 CC RELEASED.
 CC -1- MISCELLANEOUS: IC3B IS THE SLOWLY CLEAVED (POSSIBLY BY FACTOR I)
 CC TO FORM C3C AND C3DG. OTHER PROTEASES PRODUCE OTHER FRAGMENTS SUCH
 CC AS C3D OR C3G.
 CC -1- SIMILARITY: TO C4, C5 AND ALPHA-2-MACROGLOBULIN.
 CC -1- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
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 DR EMBL; K02782; AAC42013.1; -;
 DR EMBL; J00369; AAA37336.1; -;
 DR EMBL; J00367; AAA37336.1; JOINED.
 DR EMBL; M33032; AAA37378.1; -;
 DR EMBL; Z37998; CAA86099.2; -;
 DR PIR; A05290; C3MS.
 DR HSSP; P01024; IC3D.
 DR MGD; MGI:88227; C3.
 DR InterPro; IPR002890; A2M_N.
 DR InterPro; IPR001599; Alpha_2_macroglbln.
 DR InterPro; IPR000020; Anaphylatoxin.
 DR InterPro; IPR001840; Anaphylatoxn.
 DR InterPro; IPR001134; Netrin_C.
 DR Pfam; PF00207; A2M; 1.
 DR Pfam; PF01835; A2M_N; 1.
 DR Pfam; PF01821; ANATO; 1.
 DR Pfam; PF01759; NTR; 1.
 DR PRINTS; PR00004; ANAPHYLATOXN.
 DR ProDom; PD003264; Anaphylatoxin; 1.
 DR SMART; SM00104; ANATO; 1.
 DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
 KW Complement pathway; Complement alternate pathway; Plasma;
 KW Inflammatory response; Glycoprotein; Signal; Alternative initiation.
 FT SIGNAL 1 24
 FT CHAIN 25 1663 COMPLEMENT C3.
 FT CHAIN 25 666 COMPLEMENT C3, BETA CHAIN.
 FT CHAIN 671 1663 COMPLEMENT C3, ALPHA CHAIN.
 FT CHAIN 1129 1663 COMPLEMENT C3, SHORT ISOFORM.
 FT INIT_MET 1129 1129 FOR SHORT ISOFORM.
 FT PEPTIDE 671 748 C3A (ALPHA' CHAIN).
 FT CHAIN 749 1663 C3B (ALPHA' CHAIN).
 FT PEPTIDE 749 954 C3C FRAGMENT.
 FT PEPTIDE 955 1303 C3DG FRAGMENT.
 FT PEPTIDE 955 1001 C3G FRAGMENT.

RT and determination of their full-length cDNA sequences.";

RL An. J. Vet. Res. 59:704-711(1998).

CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES

CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL

CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.

CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING

CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE

CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS

CC (BY SIMILARITY).

CC -1- SUBUNIT: MONOMER (BY SIMILARITY).

CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE

CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.

CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE

CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS

CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER

CC SECRETORY PROTEINS.

CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.

CC -----

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CC -----

DR EMBL; D42146; BAA07717.1; -

DR EMBL; U92480; AAC39255.1; -

DR HSP; P01583; IITA.

DR InterPro: IPR002348; ILL_HBGF.

DR InterPro: IPR000975; Interleukin_1.

DR InterPro: IPR003502; Interleukin_1_prop.

DR Pfam: PF00340; IL1; 1.

DR Pfam: PF02394; IL1_propep; 1.

DR PRINTS: PR00262; ILL_HBGF.

DR SMART: SM00125; IL1; 1.

DR PROSITE: PS00253; INTERLEUKIN_1; 1.

DR Cytokine: Macrophage; Mitogen; Inflammatory response; Pyrogen.

FT PROPEP 1 112 BY SIMILARITY.

FT CHAIN 113 270 INTERLEUKIN-1 ALPHA.

FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CONFLICT 110 110 R -> K (IN REF. 2).

FT CONFLICT 150 150 G -> V (IN REF. 2).

FT SEQUENCE 270 AA; 30806 MW; 381859713754DB90 CRC64;

Query Match 9.5%; Score 77.5; DB 1; Length 270;

Best Local Similarity 22.3%; Pred. No. 3.4;

Matches 29; Conservative 29; Mismatches 61; Indels 11; Gaps 4;

QY 7 SKLSVIRNLNDQVLFDQGNRPFLFEDMTSDSCRONAPRTI-----FTIISMVKDSQPRGMA 61

Db 122 TKNFMIRIVNHQCTLNDALNQSVIRDTSGOYLATAALNNLDDAVKFDMDGAYTSEDSQLP 181

QY 62 VTSIV-KCEIKISTLSCENKIISPKEM-NPPDNTKDKSDIIFQTSRVPGHDKMKQFESS 119

Db 182 VTLRISKTRLFVSAQNEDEPVLLKEMPTDKTKIDETNLLFWER----HGSKNYKFSVA 237

QY 120 YEGYFLACEK 129

Db 238 HPKLFIATKQ 247

RESULT 13

OASB_MOUSE

ID OASB_MOUSE STANDARD; PRT; 192 AA.

DT Q60836;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE 2'-5'-oligoadenylate synthetase 1B (EC 2.7.7.-) ((2'-5')oligo(A)

DE synthetase 1B) (Fragment).

GN OAS1B OR OIAS2.

Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91232962; PubMed=1709495;

RA Rutherford M.N., Kumar A., Nissim A., Chebath J., Williams B.R.G.;

RT "The murine 2-5A synthetase locus: three distinct transcripts from two

RT linked genes";

RL Nucleic Acids Res. 19:1917-1924(1991).

CC -1- FUNCTION: THE 2-5A SYSTEM (THE OAS, 2-5A, AND RNASE L) MAY PLAY A

CC ROLE IN MEDIATING RESISTANCE TO VIRUS INFECTION, CONTROL OF CELL

CC GROWTH, DIFFERENTIATION, AND APOPTOSIS.

CC -1- CATALYTIC ACTIVITY: BINDS DOUBLE-STRANDED RNA AND POLYMERIZES ATP

CC INTO PPP(A2'P5'A)N OLIGOMERS, WHICH ACTIVATE THE LATENT RNASE L

CC THAT, WHEN ACTIVATED, CLEAVES SINGLE-STRANDED RNAS.

CC -1- INDUCTION: BY INTERFERONS.

CC -1- SIMILARITY: BELONGS TO THE 2-5A SYNTHETASE FAMILY.

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CC -----

DR EMBL; X55982; CAA39455.1; -

DR MGD; MGI:97430; Oas1b.

DR InterPro: IPR001797; 25A_synth.

DR InterPro: IPR001201; PAP_25A_core.

DR PROSITE: PS00832; 25A_SYNTH_1; PARTIAL.

DR PROSITE: PS00833; 25A_SYNTH_2; PARTIAL.

DR PROSITE: PS50152; 25A_SYNTH_3; 1.

KW RNA-binding; Transferase; Nucleotidyltransferase;

KW Interferon induction.

FT NON_TER 1 1

FT SEQUENCE 192 AA; 21936 MW; 4E1C011EF9024F46 CRC64;

Query Match 9.3%; Score 75.5; DB 1; Length 192;

Best Local Similarity 23.2%; Pred. No. 3.5;

Matches 42; Conservative 24; Mismatches 50; Indels 65; Gaps 9;

QY 3 GKLESKLSVIRN-----LNDQVLFDQGNRPFLFEDMTSDSCRONAPRTIIFISMVKD 54

Db 11 GRSDADLVFELNLTSTFEDLNQNGVLIKEIKKQLCVQHERRC----- 54

QY 55 SQPRGMAVTSVKCEKISTLSCENKIISPKEMNPPONIKDKTSII----- 100

Db 55 -----GVKFEVHLSRSPNSRALSFK-LSNPOLLKVEKFDVLPAYDLLOHLNLKK 103

QY 101 -----FTQF-----SYP-GHDNKKMFESSYEGYFLACE--KERDLFKLI-----LKKEDELG 145

Db 104 PNQOFYANLISGVPAKGKGLKSCFMCGLQYFLNCRPTKLRILRLVTHWYQLCKE-KLG 162

QY 146 D 146

Db 163 D 163

RESULT 14

M3K8_MOUSE

ID M3K8_MOUSE STANDARD; PRT; 467 AA.

AC Q07174;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Mitogen-activated protein kinase kinase kinase 8 (EC 2.7.1.-) (COT

DE proto-oncogene serine/threonine-protein kinase) (C-COT) (Cancer osaka

DE thyroid oncogene).

```
GN MAP3K8 OR COT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 x CBA; TISSUE=Thymus;
RX MEDLINE=93308016; PubMed=8320169;
RA Ohara R., Miyoshi J., Aoki M., Toyoshima K.;
RT "The murine cot proto-oncogene: genome structure and tissue-specific
expression.";
RL Jpn. J. Cancer Res. 84:518-525(1993).
CC -!- FUNCTION: Able to activate NF-kappa-B 1 by stimulating proteasome-
mediated proteolysis of NF-kappa-B 1/p105. Play a role in the cell
cycle (By similarity).
CC -!- SUBUNIT: Interacts with NFKB1/p105.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: High in adult submandibular gland, thymus,
spleen and newborn digestive tract.
CC -!- PTM: Autophosphorylated (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE KINASE SUBFAMILY.
CC -----
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CC -----
DR EMBL: D13759; BAA02905.1; -
DR HSP; Q00534; IBI8.
DR MGD; MGI:1346878; Map3k8.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase.1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR Transferase: Serine/threonine-protein kinase; Proto-oncogene;
ATP-binding; Phosphorylation.
DR FT DOMAIN 138 388 PROTEIN KINASE.
FT NP_BIND 144 152 ATP (BY SIMILARITY).
FT BINDING 167 167 ATP (BY SIMILARITY).
FT ACT_SITE 253 253 BY SIMILARITY.
SQ SEQUENCE 467 AA; 52941 MW; 60C2A34E530866BE CRC64;

Query Match 9.2%; Score 75; DB 1; Length 467;
Best Local Similarity 24.0%; Pred. No. 11;
Matches 29; Conservative 22; Mismatches 36; Indels 34; Gaps 6;

Qy 12 IRNLNDQVLFDGQNRPLFEDMTSDCRDNPRTIFITISMYKDSQPRGMATISVKCEKI 71
Db 361 MRELIEAALERNPNHRKPAADLLKHEAL-NPPR-----EDQPR-----CQSL 401

Qy 72 STLSCENK-IISFKEMPPNPKDT-----KSDIIFQSVPGHDKNWKOFESSSYEGY 123
Db 402 DSALFERKRLSLKQLPENIADSSCTGSTGESEVLRQR-----LYIDIGALAGY 454

Qy 124 F 124
Db 455 F 455

RESULT 15
RFL_TREPA
ID RFL_TREPA STANDARD; PRT; 351 AA.
AC O83090;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
```

```
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Peptide chain release factor 1 (RF-1).
GN PRFA OR TP0051.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NICHOLS;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
RA Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA McDonald L., Artach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
spirochete.";
RL Science 281:375-388(1998).
CC -!- FUNCTION: PEPTIDE CHAIN RELEASE FACTOR 1 DIRECTS THE TERMINATION
OF TRANSLATION IN RESPONSE TO THE PEPTIDE CHAIN TERMINATION
CODONS UAG AND UAA (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE PROKARYOTIC AND MITOCHONDRIAL RELEASE
FACTORS FAMILY.
CC -----
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CC -----
DR EMBL: AE001190; AAC65047.1; -
DR TIGR: TP0051.
DR InterPro: IPR000352; pep_rel_factor_I.
DR Pfam: PF00472; RF-1; 1.
DR PROSITE: PS00745; RF_PROK_I; 1.
DR Protein biosynthesis; Complete proteome.
SQ SEQUENCE 351 AA; 40194 MW; 6993C6F883B5797C CRC64;

Query Match 9.1%; Score 74.5; DB 1; Length 351;
Best Local Similarity 20.8%; Pred. No. 8.8;
Matches 27; Conservative 27; Mismatches 51; Indels 25; Gaps 4;

Qy 29 LFEDMTSDCRDNPRTIFITISMYKDSQPRGMATISVKCEKISTLSCENKIISFKEMNP 88
Db 64 LIQDESADAFKDVIRQEI-----RTLEAALHTSOKRLKTL-----LIP 101

Qy 89 PDNIKTPKSDIIFQSVPGHDKNWKOFESSSYEGYFLACEKRDLFKLILKKEDELGD-R 147
Db 102 PDSLQE--KNIIIMEIRGTGGDEAALFAADLFRMYTHYAESKQWRYEVLAVSETELGGFK 159

Qy 148 SIMFTVQNEED 157
Db 160 EITFTSISGRD 169

Search completed: October 8, 2002, 10:17:04
Job time: 190 sec
```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 8, 2002, 10:16:41 ; Search time 43.19 Seconds
(without alignments)
628.854 Million cell updates/sec

Title: SEQ6THRAT73
Perfect score: 816
Sequence: 1 YFGKLESLSVIRNLNDQVL.....LKKDELGDRSIMFTVQNE 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL19:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phase:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriap:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	803	98.4	193	4 Q96KJ8	Q96KJ8 homo sapien
2	797	97.7	193	6 Q9BG15	Q9BG15 macaca mula
3	659	80.8	178	6 Q9MZL8	Q9MZL8 bos taurus
4	653	80.0	193	6 Q9GL09	Q9GL09 ovis aries
5	639	78.3	192	6 Q95M33	Q95M33 felis silve
6	631	77.3	192	6 Q9N1P7	Q9N1P7 sus scrofa
7	446	54.7	196	11 Q91Z66	Q91Z66 sigmodon hi
8	318	39.0	84	6 Q95LE7	Q95LE7 canis famil
9	204	25.0	45	4 Q9NQ49	Q9NQ49 homo sapien
10	192	23.5	211	13 Q98SQ1	Q98SQ1 anas platyr
11	181.5	22.2	198	13 Q918D2	Q918D2 gallus gall
12	88	10.8	4643	5 Q9VW71	Q9VW71 drosophila
13	85	10.4	381	3 Q43031	Q43031 schizosacch
14	81.5	10.0	617	5 Q25986	Q25986 plasmodium
15	81.5	10.0	1049	2 Q93KF0	Q93KF0 caldicellul
16	81	9.9	263	3 Q74316	Q74316 schizosacch

17	80.5	9.9	866	16	O84500	chlamydia t
18	80	9.8	2470	13	Q90681	gallus gall
19	79.5	9.7	1044	3	Q94173	pneumocysti
20	79	9.7	452	16	O25249	helicobacte
21	78.5	9.6	204	2	Q9ZNU7	clostridium
22	78.5	9.6	595	10	Q9SDM4	dunaliella
23	78	9.6	473	5	O16673	caenorhabdi
24	77.5	9.5	454	6	Q9BGD1	micronycter
25	77.5	9.5	840	12	Q9QBA2	yaba monkey
26	77.5	9.5	1251	13	Q91365	cuturnix co
27	77	9.4	364	16	Q9PM33	campylobact
28	77	9.4	847	4	Q9NUC1	homo sapien
29	76.5	9.4	425	5	P90990	caenorhabdi
30	76.5	9.4	454	6	Q9BGA8	sturnira li
31	76	9.3	632	10	O80569	arabidopsis
32	76	9.3	747	10	O82393	arabidopsis
33	75.5	9.3	454	6	Q9BGE4	erophyllia s
34	75.5	9.3	454	6	Q9BGB7	phylostoma
35	75.5	9.3	578	16	Q9PPR7	ureaplasma
36	75	9.2	445	13	O57610	scyllorhinu
37	75	9.2	1064	13	Q90601	gallus gall
38	75	9.2	1247	5	Q95QV2	caenorhabdi
39	74.5	9.1	137	5	O77077	plasmodium
40	74.5	9.1	334	10	Q9ZSB9	arabidopsis
41	74.5	9.1	454	6	Q9BGB8	phyllonycte
42	74.5	9.1	454	6	Q9BGB1	saccolaryx
43	74.5	9.1	974	11	Q924W2	rattus norv
44	74.5	9.1	1510	5	Q22699	caenorhabdi
45	74	9.1	245	17	Q97UG0	sulfolobus

ALIGNMENTS

RESULT 1

ID Q96KJ8 PRELIMINARY; PRT; 193 AA.
AC Q96KJ8;
DT 01-DEC-2001 (TREMREL. 19, Created)
DT 01-DEC-2001 (TREMREL. 19, Last sequence update)
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
DE INTERLEUKIN 18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ying P., Jianxin L.;
RT "Cloning of Mutant Human Interleukin 18 cDNA";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF380360; AAK57024.1; ...
SQ SEQUENCE 193 AA; 22323 MW; 2E500205D1B7E5F7 CRC64;

Query Match	98.4%	Score 803;	DB 4;	Length 193;
Best Local Similarity	98.1%	Pred. No. 2.9e-73;		
Matches 154;	Conservative 2;	Mismatches 1;	Indels 0;	Gaps 0;
Qy 1	YFGKLESLSVIRNLNDQVLFDQGNRPLFEDMTDSCRDNAPRTIFIIISMYKDSQPRGM	60		
Db 37	YFGKLESLSVIRNLNNQVLFDQGNRPLFEDMTDSCRDNAPRTIFIIISMYKDSQPRGM	96		
Qy 61	AVTISVKEKISTLSCEKNKISFKEMNPPDNITKOTKDSIIFFQFQSVPGHDNKMQFESSY	120		
Db 97	AVTISVKEKISTLSCEKNKISFKEMNPPDNITKOTKDSIIFFQFQSVPGHDNKMQFESSY	156		
Qy 121	EGYFLACEKERDLFLKLLKKEDELGDRSIMFTVQNE 157			
Db 157	EGYFLACEKERDLFLKLLKKEDELGDRSIMFTVQNE 193			
RESULT 2				


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Q9NQ49
ID Q9NQ49 PRELIMINARY; PRT; 45 AA.
AC Q9NQ49
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE INTERLEUKIN-18 (FRAGMENT).
GN IL-18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Farhan A.J., Pravica V., Hutchinson I.V.;
RT "Identification of Human Interleukin-18 gene polymorphisms.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ295724; CAC01436.1; -.
FT NON_TER 1 45
FT NON_TER 45 45
SQ SEQUENCE 45 AA; 5266 MW; DF3A626507E3D61A CRC64;

Query Match 25.0%; Score 204; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.4e-13;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLVIRNLNDQVLFDIOGGRPLFEDMTDSDCR 39
Db 7 YFGKLESKLVIRNLNDQVLFDIOGGRPLFEDMTDSDCR 45

RESULT 10
Q98SQ1
ID Q98SQ1 PRELIMINARY; PRT; 211 AA.
AC Q98SQ1
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DE INTERLEUKIN-18 (FRAGMENT).
GN IL-18.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RA Chan W.-S., Warr G.W., Middleton D.L., Lundquist M.L., Higgins D.A.;
RT "Anas platyrhynchos T-cell antigens, IL-18 gene.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF336122; AAK26322.1; -.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 211 AA; 24541 MW; CA6FC63538211B2B CRC64;

Query Match 23.5%; Score 192; DB 13; Length 211;
Best Local Similarity 36.5%; Pred. No. 1.4e-11;
Matches 61; Conservative 29; Mismatches 63; Indels 14; Gaps 9;

QY 2 FGKLESKLVIRNLNDQVLFDIOG-NRPLFEDMTDSDCRNAPRTIFIISMVKDSQP-RG 59
Db 43 FSKEKTLHRLNRVNSQVLVVRPDLNVAAFEDVTDQEKSGSGMN-FCMHCYKTTTPSAG 101

QY 60 MAVTISVKCE-KISTLSCENK-----IISFKEMNPPDNKDKSDIIFQSRVPGHDNK-M 113
Db 102 MPVAFSRVEDKSYMCCEEHGKMIVRFREGEVPKDIPG-ESNIIFPKTFTSYSSKAF 160

QY 114 QFESSSYEGYFLACEKRDLPKLLKK---EDELGDRS-IMFTVQNE 156
Db 161 KFEYSLGRGFLAFEEEDSLRKLILKLPREDEVDETTKITLTSHNE 207

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RESULT 11
Q918D2
ID Q918D2 PRELIMINARY; PRT; 198 AA.
AC Q918D2
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INTERLEUKIN 18.
GN IL-18.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Schneider K., Puehler F., Baeuerle D., Elvers S., Staeheli P.,
RA Kaspers B., Weining K.C.;
RT "cDNA cloning of biologically active chicken Interleukin-18.";
RL J. Interferon Cytokine Res. 20:879-883(2000).
DR EMBL; AJ277865; CAB96214.1; -.
FT CHAIN 30 198 INTERLEUKIN 18.
FT CHAIN 30 198 INTERLEUKIN 18.
SQ SEQUENCE 198 AA; 22918 MW; 29BB77DC3E3C6600 CRC64;

Query Match 22.2%; Score 181.5; DB 13; Length 198;
Best Local Similarity 36.8%; Pred. No. 1.4e-10;
Matches 57; Conservative 25; Mismatches 60; Indels 13; Gaps 7;

QY 13 RNLDQVLFDIOG-NRPLFEDMTDSDCRNAPRTIFIISMVKDSQP-RGMVATISVKCEK 70
Db 42 RNVNSQLLVVRPDLNVAAFEDVTDQEVKSGS-GMYFDHCYKTTAPSGMPVAFSVQVED 100

QY 71 ISTLSCENK-----IISFKEMNPPDNKDKSDIIFQSRVPGHDNK-MQFESSSYEGYF 124
Db 101 KSYVMCEKEHGKMIVRFREGEVPKDIPG-ESNIIFPKTFTSCSKAFKFEYSLEQGMF 159

QY 125 LACEKERDLPKLLKK---EDELGDRS-IMFTVQNE 156
Db 160 LAFEEDSLRKLILKLPREDEVDETTKFVTSHNE 194

RESULT 12
Q9VW71
ID Q9VW71 PRELIMINARY; PRT; 4643 AA.
AC Q9VW71
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE PUTATIVE FAT-LIKE CADHERIN PRECURSOR (CG7749 PROTEIN).
GN CG7749.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Fandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt J.G., Nelson C.R., Miklos G.L.G.,
RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

```

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier A., Fleischmann W.,
 RA Foshier C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Wellesbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: MAY BE INVOLVED IN CELL ADHESION.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
 CC -1- SIMILARITY: CONTAINS 5 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 LAMININ G-LIKE DOMAIN.
 DR EMBL: AE003515; AAF49078.1; -;
 DR HSP: P15116; INCI
 DR FlyBase: FBgn0036930; fat2.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR002126; Cadherin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR001791; Laminin_G.
 DR Pfam: PF00028; cadherin; 33.
 DR Pfam: PF00008; EGF; 5.
 DR Pfam: PF00054; laminin_G; 1.
 DR PRINTS: PR00205; CADHERIN.
 DR SMART: SM00112; CA; 33.
 DR SMART: SM00179; EGF_CA; 1.
 DR SMART: SM00001; EGF_Like; 5.
 DR SMART: SM00282; LamG; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 DR PROSITE: PS00232; CADHERIN_1; 1.
 DR PROSITE: PS02568; CADHERIN_2; 41.
 DR PROSITE: PS00022; EGF_1; 5.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA; 1.
 KW Hypothetical protein; Cell adhesion; Signal; Transmembrane; Repeat;
 KW EGF-like domain; Glycoprotein; Calcium-binding.
 FT SIGNAL 1 35
 FT CHAIN 36 4643
 FT DOMAIN 36 1647
 FT TRANSMEM 1648 1668
 FT DOMAIN 1669 1699
 FT DOMAIN 1699 1800
 FT DOMAIN 1800 1899
 FT DOMAIN 1899 2000
 FT DOMAIN 2000 2100
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OM protein - protein search, using sw model

Run on: October 8, 2002, 10:14:17 ; Search time 20.63 seconds
(without alignments)
185.886 Million cell updates/sec

Title: SEQ6THRAT73

Perfect score: 816

Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LAKKDELGDRSIMFTVQNE 157

Scoring table: BLOSUM62

Gapop 10.0 , Capext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA.*

1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*

2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*

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6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	811	99.4	157	2	US-08-896-605A-6
2	811	99.4	157	2	US-08-896-501A-4
3	811	99.4	157	3	US-08-884-324-1
4	811	99.4	157	3	US-08-996-338-26
5	811	99.4	157	4	US-08-558-818-1
6	811	99.4	157	4	US-08-974-469A-1
7	811	99.4	157	4	US-08-832-180-1
8	811	99.4	157	4	US-08-832-198-6
9	811	99.4	193	2	US-08-896-605A-2
10	811	99.4	193	4	US-08-896-501A-2
11	811	99.4	193	4	US-08-832-180-9
12	518	63.5	157	2	US-08-502-535B-2
13	518	63.5	157	2	US-08-908-005A-2
14	518	63.5	157	3	US-08-996-338-27
15	518	63.5	157	4	US-08-558-818-7
16	518	63.5	157	4	US-08-974-469A-7
17	518	63.5	157	4	US-08-832-180-8
18	518	63.5	157	4	US-08-832-198-11
19	518	63.5	157	4	US-08-253-523-2
20	518	63.5	157	4	US-08-251-911-2
21	259	31.7	50	4	US-08-832-198-2
22	96	11.8	25	4	US-08-558-818-4
23	96	11.8	25	4	US-08-974-469A-4
24	96	11.8	25	4	US-08-832-180-4
25	96	11.8	25	4	US-08-832-198-8
26	90	11.0	17	4	US-08-832-198-5
27	81	9.9	155	6	5494663-8

28	81	9.9	267	6	5494663-5	Patent No. 5494663
29	77.5	9.5	270	2	US-08-611-880-1	Sequence 1, Appl
30	77.5	9.5	270	4	US-09-085-305-13	Sequence 13, Appl
31	75.5	9.3	270	4	US-09-085-305-20	Sequence 20, Appl
32	74	9.1	270	4	US-09-085-305-14	Sequence 14, Appl
33	73.5	9.0	855	2	US-08-482-090-12	Sequence 12, Appl
34	73.5	9.0	856	2	US-08-481-700B-8	Sequence 8, Appl
35	73.5	9.0	856	2	US-09-007-383-16	Sequence 16, Appl
36	72.5	8.9	268	4	US-09-085-305-8	Sequence 8, Appl
37	72.5	8.9	268	4	US-09-085-305-18	Sequence 18, Appl
38	72.5	8.9	1294	2	US-08-819-288-3	Sequence 3, Appl
39	72.5	8.9	1294	4	US-09-400-348-3	Sequence 3, Appl
40	72.5	8.9	1321	1	US-08-261-822A-3	Sequence 3, Appl
41	72.5	8.9	1321	5	PCT-US95-07744A-3	Sequence 3, Appl
42	71.5	8.8	268	4	US-09-085-305-10	Sequence 10, Appl
43	71.5	8.8	3418	3	US-08-755-587-44	Sequence 44, Appl
44	71	8.7	14	4	US-08-832-198-4	Sequence 4, Appl
45	71	8.7	1588	5	PCT-US93-07261-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-896-605A-6
; Sequence 6, Application US/08896605A
; Patent No. 5879942
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896.605A
; FILING DATE: 18 July 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 207.691/1996
; FILING DATE: 19-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 156.062/1997
; FILING DATE: 30-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-896-605A-6

Query Match 99.4%; Score 811; DB 2; Length 157;
Best Local Similarity 99.4%; Pred. No. 5.4e-88;
Matches 156; Conservative 1; Indels 0; Gaps 0;

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Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIISMYKDSQPRGM 60
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QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTSDIIFQSVPGHDKNMQFESSY 120
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Db 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTSDIIFQSVPGHDKNMQFESSY 120
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QY 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157
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Db 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157
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RESULT 2
US-08-896-501A-4
; Sequence 4, Application US/08896501A
; Patent No. 5891663
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,501A
; FILING DATE: 18-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 213,267/1996
; FILING DATE: 25-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 31,474/1997
; FILING DATE: 31-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO-3
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-896-501A-4

Query Match 99.4%; Score 811; DB 2; Length 157;
Best Local Similarity 99.4%; Pred. No. 5.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTSDIIFQSVPGHDKNMQFESSY 120
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Db 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTSDIIFQSVPGHDKNMQFESSY 120
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QY 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157
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Db 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157
|||||
RESULT 3
US-08-884-324-1
; Sequence 1, Application US/08884324
; Patent No. 6060283
; GENERAL INFORMATION:
; APPLICANT: Takanori OKURA
; APPLICANT: Kakuji TORIGOE
; APPLICANT: Masahi KURIMOTO
; TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
; OF INDUCING THE PRODUCTION OF INTERFERON-
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/884,324
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 185,305/96
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: OKURA-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-884-324-1

Query Match 99.4%; Score 811; DB 3; Length 157;
Best Local Similarity 99.4%; Pred. No. 5.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIISMYKDSQPRGM 60
|||||
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIISMYKDSQPRGM 60
|||||
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTSDIIFQSVPGHDKNMQFESSY 120
|||||
Db 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTSDIIFQSVPGHDKNMQFESSY 120
|||||
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157
|||||
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157
|||||
RESULT 4
US-08-996-338-26
; Sequence 26, Application US/08996338
; Patent No. 6087116
; GENERAL INFORMATION:

APPLICANT: TORIGOE, Kakuji
APPLICANT: OKURA, Takanori
TITLE OF INVENTION: KURIMOTO, Masashi
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996.338
FILING DATE: 22-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74,697/1997
FILING DATE: 12-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 215,488/1997
FILING DATE: 28-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 291,837/1997
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 157
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-996-338-26

Query Match 99.4%; Score 811; DB 3; Length 157;
Best Local Similarity 99.4%; Pred. No. 5.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNRNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNRNAPRTIFIISMYKDSQPRGM 60
Qy 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNKDKTSIIFFQRSVPVGHDKNMQFESSY 120
Db 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNKDKTSIIFFQRSVPVGHDKNMQFESSY 120
Qy 121 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNEED 157

RESULT 5
US-08-558-818-1
Sequence 1, Application US/08558818
Patent No. 6197297
GENERAL INFORMATION:
APPLICANT:
APPLICANT: NAME: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENKYUJO
APPLICANT: KUNIKATA, Toshio
APPLICANT: TANIGUCHI, Mutsuko
APPLICANT: KOHNO, Keizo

APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
TITLE OF INVENTION: WHICH INDUCES INTERFERON- PRODUCTION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: FELICI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/558.818
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA: JP 58,240/95
PRIOR APPLICATION DATA: February 23, 1995
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-558-818-1

Query Match 99.4%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 5.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNRNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNRNAPRTIFIISMYKDSQPRGM 60
Qy 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNKDKTSIIFFQRSVPVGHDKNMQFESSY 120
Db 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNKDKTSIIFFQRSVPVGHDKNMQFESSY 120
Qy 121 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNEED 157

RESULT 6
US-08-974-469A-1
Sequence 1, Application US/08974469A
Patent No. 6207641
GENERAL INFORMATION:
APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENKYUJO
APPLICANT: TORIGOE, Kakuji
APPLICANT: TANIMOTO, Tadao
APPLICANT: FUKUDA, Shigeharu
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: AGENT FOR SUSCEPTIVE DISEASE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,469A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/599,879
FILING DATE:
APPLICATION NUMBER: JP 78,357/95
FILING DATE: March 10, 1995
APPLICATION NUMBER: JP 274,988/95
FILING DATE: September 29, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOB-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-469A-1

Query Match 99.4%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 5.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM 60
DB 1 YFGKLESKLVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKMKQFESSY 120
DB 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSINFTVQNE 157
DB 121 EGYFLACEKERDLFKLLKKEDELGDRSINFTVQNE 157

RESULT 7
US-08-832-180-1
Sequence 1, Application US/08832180
Patent No. 6214584
GENERAL INFORMATION:
APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENYUJO
APPLICANT: USHIO, Shimpel
APPLICANT: TORIGOE, Kakuji
APPLICANT: TANIMOTO, Tadao
APPLICANT: OKAMURA, Haruki
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: INTERFERON- PRODUCTION INDUCING
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA

ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,180
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/558,191
FILING DATE:
APPLICATION NUMBER: JP 304,203/94
FILING DATE: No. 6214584ember 15, 1994
APPLICATION NUMBER: 10048102
FILING DATE: September 18, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: USHIO-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-832-180-1

Query Match 99.4%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 5.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM 60
DB 1 YFGKLESKLVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKMKQFESSY 120
DB 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSINFTVQNE 157
DB 121 EGYFLACEKERDLFKLLKKEDELGDRSINFTVQNE 157

RESULT 8
US-08-832-198-6
Sequence 6, Application US/08832198
Patent No. 6242255
GENERAL INFORMATION:
APPLICANT: AKITA, Kenji
APPLICANT: NUKADA, Yoshiyuki
APPLICANT: FUJII, Mitsukiyo
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,198
FILING DATE: 08-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/721,018
FILING DATE: 25-SEP-1996
APPLICATION NUMBER: JP 95-270725
FILING DATE: 26-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 96-067434
FILING DATE: 29-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP not yet received
FILING DATE: 20-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: AKITA-1
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: "Xaa" in position 73 is either
OTHER INFORMATION: 'Ile' or 'Thr'
US-08-832-198-6

Query Match 99.4%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 5.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Qy 61 AVTISVCKEISTLSKCNKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 120
Db 61 AVTISVCKEISTLSKCNKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 9
US-08-896-605A-2
Sequence 2, Application US/08896605A
Patent No. 5879942
GENERAL INFORMATION:
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,605A
FILING DATE: 18 JULY 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 207,691/1996
FILING DATE: 19-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 156,062/1997
FILING DATE: 30-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TANIMOTO-2
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-896-605A-2
Query Match 99.4%; Score 811; DB 2; Length 193;
Best Local Similarity 99.4%; Pred. No. 7.2e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 96
Qy 61 AVTISVCKEISTLSKCNKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 120
Db 97 AVTISVCKEISTLSKCNKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 156
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193
RESULT 10
US-08-896-501A-2
Sequence 2, Application US/08896501A
Patent No. 5891663
GENERAL INFORMATION:
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,501A
FILING DATE: 18-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 213,267/1996
FILING DATE: 25-JUL-1996

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 31,474/1997
; FILING DATE: 31-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, ROGER L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-896-501A-2

Query Match 99.4%; Score 811; DB 2; Length 193;
Best Local Similarity 99.4%; Pred. No. 7.2e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60
|||||
Db 37 YFGKLESLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 96
QY 61 AVTISVKEKISTLSCENKIISFKEMNPPDNKTDSIIFFQRSVPGHNDKMQPESY 120
|||||
Db 97 AVTISVKEKISTLSCENKIISFKEMNPPDNKTDSIIFFQRSVPGHNDKMQPESY 156
QY 121 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNE 157
|||||
Db 157 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNE 193

RESULT 11
US-08-832-180-9
; Sequence 9, Application US/08832180
; Patent No. 6214584
; GENERAL INFORMATION:
; APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
; APPLICANT: KENYUJO
; APPLICANT: USHIO, Shimpai
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: OKAMURA, Haruki
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: INTERFERON- PRODUCTION INDUCING
; TITLE OF INVENTION: POLYPEPTIDE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect Version 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832,180
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/558,191
; FILING DATE:
; APPLICATION NUMBER: JP 304,203/94
; FILING DATE: No. 6214584ember 15, 1994

; APPLICATION NUMBER: 10048102
; FILING DATE: September 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: USHIO-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-832-180-9

Query Match 99.4%; Score 811; DB 4; Length 193;
Best Local Similarity 99.4%; Pred. No. 7.2e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60
|||||
Db 37 YFGKLESLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 96
QY 61 AVTISVKEKISTLSCENKIISFKEMNPPDNKTDSIIFFQRSVPGHNDKMQPESY 120
|||||
Db 97 AVTISVKEKISTLSCENKIISFKEMNPPDNKTDSIIFFQRSVPGHNDKMQPESY 156
QY 121 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNE 157
|||||
Db 157 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNE 193

RESULT 12
US-08-502-535B-2
; Sequence 2, Application US/08502535B
; Patent No. 5912324
; GENERAL INFORMATION:
; APPLICANT: OKAMURA, Haruki
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: KUNIKATA, Toshio
; APPLICANT: TANIGUCHI, Mutsuko
; APPLICANT: KOHNO, Keizo
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: IFN-BETA PRODUCTION INDUCING PROTEIN AND
; TITLE OF INVENTION: MONOCLONAL ANTIBODY OF THE SAME
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/502,535B
; FILING DATE: 14-JUL-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 184162/1994
; FILING DATE: 14-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 45057/1995
; FILING DATE: 10-FEB-1995

```

: ATTORNEY/AGENT INFORMATION:
: NAME: BROWDY, Roger L.
: REGISTRATION NUMBER: 25,618
: REFERENCE/DOCKET NUMBER: OKAMURA-2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-628-5197
: TELEFAX: 202-737-3528
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 157 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-052-535B-2

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	Query Match	63.5%	Score 518;	DB 2;	Length 157;
	Best Local Similarity	65.6%;	pred. No. 1.8e-53;		
	Matches 101;	Conservative 26;	Mismatches 25;	Indels 2;	Gaps 2;
Qy	2	FGKLESLSVRNLDQVLFIDOGNRPLFEDMTSDCRONAPRTIFILSMYKDSPRGMA	61		
Db	2	FGRUHCCTAVIRNLDQVLFVDK-RQPVEFDMTDIDQSASEPQTLLIIMYKDSVRGLA	60		
Qy	62	VTSIVKCEKISTLSCENKIISFKEMNPNDIKTKDSIIFFQRSVPGHDKMKOFESSSYE	121		
Db	61	VTLVSOKSKSTLSCKNKIIISFEEMDPDENDDIQSDLIFFQKRYPGH-NKMEPESSLYE	119		
Qy	122	GYFLACSKERDLFKLILKKEDELGDGRSImFTVQN	155		
Db	120	GHFLLACQEKEDDAFKLILKKDENGDKSVWFtLTN	153		

RESULT 13
US-08-908-005A-2
; Sequence 2, Application US/08908005A
; Patent No. 5914253
; GENERAL INFORMATION:
; APPLICANT: OKAMURA, Haruki
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: KUNIKATA, Toshio
; APPLICANT: TANIGUCHI, Mutsuko
; APPLICANT: KOHNO, Keizo
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: IFN-BETA PRODUCTION INDUCING PROTEIN AND
; TITLE OF INVENTION: MONOCLONAL ANTIBODY OF THE SAME
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,005A
; FILING DATE: 11-AUG-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/502,535
; FILING DATE: 14-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 184162/1994
; FILING DATE: 14-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 45057/1995
; FILING DATE: 10-FEB-1995

```

;
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: OKAMURA-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-908-005A-2

Query Match 63.5%; Score 518; DB 2; Length 157;
Best Local Similarity 65.6%; Pred. No. 1.8e-53;
Matches 101; Conservative 26; Mismatches 25; Indels 2; Gaps 61

Qy 2 FGLKLEKSLVIRNLNDQVLFDIGNRPFLFEDMTDSDCRNAPRTFIISMYKDSQPRGMA 61
   ||| :|||:|||||: :|:||||| :|:| ||||| :|:|
Db 2 FGLRHCTTAVIRNLNDQVLVDK-RQPVEDMTDIDQASASEPQTRLIIYMYKDSVVRGLA 60

Qy 62 VTSVCKEKTSLSCENKIISFKEMAPPDNKIKTSIDITFFQRSVPGHKNKQFESSYSYE 121
   |||:| |||||:|||||:|||||:| :||:||||: |||:||||| |||:|||||
Db 61 VTLVSVDKSKYTSCKNKIISFEEMPPENIDDIQSDLIFFQKRVPGH-NKMEFESSLYE 119

Qy 122 GYFLACEKERDLFKLILKKDELDGDRSIMETVON 155
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Db 120 GHFLAQKEDDAFKLILKKDENGSKSVMTLTN 153

RESULT 14
US-08-996-338-27
; Sequence 27, Application US/08996338
; Patent No. 608716
; GENERAL INFORMATION:
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: OKURA, Takanori
; APPLICANT: KURIMOTO, Musashi
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; City: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,338
; FILING DATE: 22-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 74,697/1997
; FILING DATE: 12-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 215,488/1997
; FILING DATE: 28-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 291,837/1997
; FILING DATE: 09-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TORIGOE-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197

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; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-996-338-27

Query Match 63.5%; Score 518; DB 3; Length 157;
Best Local Similarity 65.6%; Pred. No. 1.8e-53;
Matches 101; Conservative 26; Mismatches 25; Indels 2; Gaps 2;
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Db 2 FGRHCTTAVIRNINDQVLFDVK-RQPVFEDMTDIDQASASEPQTRLIIYMYKDSVRGLA 60
Qy 62 VTISVKCEKISLSCENKIISFKENPPDNKDTKSDIFFORSVPGHDNKNQFESSSVE 121
Db 61 VTLVKDSKXSTLSCNKKIISFEEDPPENIDDIQSDLIFFQKRVPGH-NKMEFESSLYE 119
Qy 122 GYFLACERDLFKLILKKEDELGRSMTFTVN 155
Db 120 GHFLACQEDDAFKLILKKEDEGDKSVMTLTN 153

RESULT 15
US-08-558-818-7
; Sequence 7, Application US/08558818
; Patent No. 6197297
; GENERAL INFORMATION:
; APPLICANT: NAME:KARUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
; APPLICANT: KENKYUJO
; APPLICANT: KONIKATA, Toshio
; APPLICANT: TANIGUCHI, Mutsuko
; APPLICANT: KOHNO, Keizo
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
; WHICH INDUCES INTERFERON- PRODUCTION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect Version 5.0
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: FELICI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/558,818
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: JP 58,240/95
; PRIOR APPLICATION DATA: February 23, 1995
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: mouse
; INDIVIDUAL ISOLATE: liver
US-08-558-818-7
Query Match 63.5%; Score 518; DB 4; Length 157;
Best Local Similarity 65.6%; Pred. No. 1.8e-53;
Matches 101; Conservative 26; Mismatches 25; Indels 2; Gaps 2;
Qy 2 FCKLESKLSVIRNLNDQVLFDQGNRPFLFEDMTSDCRDNAPRTIFIISMVKDSOPRGWA 61
Db 2 FGRHCTTAVIRNINDQVLFDVK-RQPVFEDMTDIDQASASEPQTRLIIYMYKDSVRGLA 60
Qy 62 VTISVKCEKISLSCENKIISFKENPPDNKDTKSDIFFORSVPGHDNKNQFESSSVE 121
Db 61 VTLVKDSKXSTLSCNKKIISFEEDPPENIDDIQSDLIFFQKRVPGH-NKMEFESSLYE 119
Qy 122 GYFLACERDLFKLILKKEDELGRSMTFTVN 155
Db 120 GHFLACQEDDAFKLILKKEDEGDKSVMTLTN 153

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Job time: 529 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 8, 2002, 10:10:39 ; Search time 51.43 Seconds
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Title: SEQ6ILEAT73

Perfect score: 815

Sequence: 1 YFGKLESLKSVIRNLNDQVL.....LKKEDELGRSIMEFTVQNED 157

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	810	99.4	157	17 AAR99564	Human interferon-g
2	810	99.4	157	17 AAR99558	Human mature inter
3	810	99.4	157	18 AAW15701	Interferon-gamma 1
4	810	99.4	157	18 AAW24258	Human protein for
5	810	99.4	157	19 AAW77158	Human interleukin-
6	810	99.4	157	19 AAW77077	Human interleukin
7	810	99.4	157	19 AAW63810	Human IL-18 protei
8	810	99.4	157	19 AAW37741	IFN-gamma inducin
9	810	99.4	157	19 AAW52176	Interferon-gamma 1
10	810	99.4	157	20 AAY39799	Interleukin-18 rec
11	810	99.4	157	21 AAY44597	Human interleukin-

12	810	99.4	157	21 AAY53904	Sequence of a matu
13	810	99.4	157	21 AAY57570	Human interleukin
14	810	99.4	157	22 AAE06661	Human interleukin-
15	810	99.4	157	22 AAB82408	Human interleukin-
16	810	99.4	157	22 AAG65294	Human interleukin-
17	810	99.4	157	22 AAG65351	Human interleukin-
18	810	99.4	158	21 AAY85167	Human interleukin-
19	810	99.4	180	19 AAW48959	Wild-type human in
20	810	99.4	193	17 AAR99560	Human interferon-g
21	810	99.4	193	18 AAW22047	Interferon-gamma 1
22	810	99.4	193	19 AAW37740	Interferon-gamma 1
23	810	99.4	193	19 AAW52172	Interferon-gamma 1
24	810	99.4	193	19 AAW47429	Interferon-gamma p
25	810	99.4	193	19 AAW46592	Amino acid sequenc
26	810	99.4	193	21 AAY53908	Amino acid sequenc
27	810	99.4	193	22 AAB82409	Human interleukin-
28	810	99.4	193	22 AAB30541	A human IL-18 with
29	810	99.4	193	22 AAG63830	Amino acid sequenc
30	807	99.0	193	19 AAW77082	Interleukin 18 act
31	802	98.4	193	18 AAW31757	Interferon gamma 1
32	800	98.2	157	19 AAW77083	Human interleukin
33	800	98.2	157	19 AAW48961	Mutant human inter
34	800	98.2	181	21 AAB23797	Human interleukin
35	791	97.1	193	22 AAY72608	Macaca cynomolgus
36	790	96.9	157	19 AAW77084	Human interleukin
37	790	96.9	157	19 AAW77085	Human interleukin
38	790	96.9	157	19 AAW48962	Mutant human inter
39	790	96.9	157	19 AAW48963	Mutant human inter
40	781	95.8	157	19 AAW77080	Human interleukin
41	781	95.8	157	19 AAW77088	Human interleukin
42	781	95.8	157	19 AAW48966	Mutant human inter
43	780	95.7	157	19 AAW77086	Human interleukin
44	780	95.7	157	19 AAW48964	Mutant human inter
45	771	94.6	157	19 AAW77081	Human interleukin

ALIGNMENTS

RESULT 1
AAR99564
ID AAR99564 standard; Protein; 157 AA.
XX AC
XX AAR99564;
XX
DT 29-SEP-1996 (first entry)
XX
DE Human interferon-gamma inducer protein.
XX
KW Interferon-gamma inducer protein; IFN-gamma; antiviral; virucide;
KW antitumour; antibacterial; immunoregulator; adoptive immunotherapy;
KW therapy; cancer.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 73
FT /label= Ile, Thr
XX
PN EP712931-A2.
XX
PD 22-MAY-1996.
XX
PF 10-NOV-1995; 95EP-0308055.
XX
PR 29-SEP-1995; 95JP-0274988.
PR 15-NOV-1994; 94JP-0304203.
PR 23-FEB-1995; 95JP-0058240.
PR 10-MAR-1995; 95JP-0078357.
PR 18-SEP-1995; 95JP-0262062.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX

PI Fukuda S, Kohno K, Kunikata T, Kurimoto M, Okamura H;
 PI Taniguchi M, Tanimoto T, Torigoe K, Ushio S;
 DR WPI: 1996-252837/26.
 DR N-PSDB; AAT32411.
 XX
 PT DNA encoding interferon-gamma prodn.-inducing polypeptide - useful
 PT to treat and prevent, e.g. viral disease, malignancies and immune
 PT disorders
 XX
 PS Example B-1-1; Page 28; 48pp; English.
 XX
 CC A novel human protein (AAR99564) that induces interferon-gamma
 CC (IFN-gamma) prodn. by immunocompetent cells is the product of a
 CC phage cDNA clone (AAT32411) derived from a human liver library.
 CC PCR amplification of the cDNA (see also AAT32409-10) and expression
 CC in Escherichia coli XL-1 Blue MRF⁺kan allowed prodn. of recombinant
 CC inducer protein. This was used to construct hybridoma H-1, which
 CC produced anti-IFN-gamma inducer protein monoclonal antibody H-1mAb,
 CC useful in the detection and purification of the inducer protein
 CC (see also AAR99558).
 XX
 SQ Sequence 157 AA;

Query Match 99.4%; Score 810; DB 17; Length 157;
 Best Local Similarity 99.4%; Pred. No. 8.1e-83;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLEFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1 yfgkleskslsvirnlndqvlfidqgnrpfedmtsdcdndaprtifiismykdsgprgm 60

QY 61 AVTISVKCEKISILSCENKIISFKEMNPPDNKDKSDIIFFORSVPGHDKMQFESSY 120
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 61 avtisvkcekisxlscenkliisfkenmpdpndkdktsdliifqrsvpgdhdkmqfessy 120

QY 121 EGYFLACERDLFKLILKKKEDELGDRSIMFTVQNE 157
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 121 egyflacekerdlfkilkkkedelgrsimftvqned 157

RESULT 2
 AAR99558
 ID AAR99558 standard; Protein; 157 AA.
 XX
 AC AAR99558;
 XX
 DT 29-SEP-1996 (first entry)
 XX
 DE Human mature interferon-gamma inducer protein.
 XX
 KW Interferon-gamma inducer protein; IFN-gamma; antiviral; virucide;
 KW antitumour; antibacterial; immunoregulator; adoptive immunotherapy;
 KW therapy; cancer.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 73
 FT /label= Ile, Thr
 XX
 PN EP712931-A2.
 XX
 PD 22-MAY-1996.
 XX
 PF 10-NOV-1995; 95EP-0308055.
 XX
 PR 29-SEP-1995; 95JP-0274988.
 PR 15-NOV-1994; 94JP-0304203.
 PR 23-FEB-1995; 95JP-0058240.
 PR 10-MAR-1995; 95JP-0078357.
 PR 18-SEP-1995; 95JP-0262062.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 PA
 XX Fukuda S, Kohno K, Kunikata T, Kurimoto M, Okamura H;
 PI Taniguchi M, Tanimoto T, Torigoe K, Ushio S;
 PI WPI: 1996-252837/26.
 XX N-PSDB; AAT32402.
 DR
 DR DNA encoding interferon-gamma prodn.-inducing polypeptide - useful
 PT to treat and prevent, e.g. viral disease, malignancies and immune
 PT disorders
 XX
 PS Claim 1; Page 40; 48pp; English.
 XX
 CC A novel human protein (AAR99558) induces interferon-gamma (IFN-gamma)
 CC prodn. by immunocompetent cells. It enhances the cytotoxicity of
 CC killer cells and/or induces the formation of killer cells (e.g.
 CC NK cells, lymphokine-activating killer (LAK) cells, and cytotoxic
 CC T-cells). Recombinant IFN-gamma inducer protein can be produced in
 CC high yields using host cells, esp. Escherichia coli, transformed
 CC with a vector carrying the encoding cDNA (AAT32402). It is useful
 CC as an antiviral, antitumor, antibacterial, immunoregulatory and
 CC blood platelet enhancing agent, and can be used in adoptive
 CC immunotherapy. It is also used to raise monoclonal antibodies.
 CC A full-length sequence is given in AAR99560.
 XX
 SQ Sequence 157 AA;

Query Match 99.4%; Score 810; DB 17; Length 157;
 Best Local Similarity 99.4%; Pred. No. 8.1e-83;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLEFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1 yfgkleskslsvirnlndqvlfidqgnrpfedmtsdcdndaprtifiismykdsgprgm 60

QY 61 AVTISVKCEKISILSCENKIISFKEMNPPDNKDKSDIIFFORSVPGHDKMQFESSY 120
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 61 avtisvkcekisxlscenkliisfkenmpdpndkdktsdliifqrsvpgdhdkmqfessy 120

QY 121 EGYFLACERDLFKLILKKKEDELGDRSIMFTVQNE 157
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 121 egyflacekerdlfkilkkkedelgrsimftvqned 157

RESULT 3
 AAW15701
 ID AAW15701 standard; protein; 157 AA.
 XX
 AC AAW15701;
 XX
 DT 26-JAN-1998 (first entry)
 XX
 DE Interferon-gamma inducer protein.
 XX
 KW Interferon-gamma, IFN-gamma; antiviral; antioncotic; radiotherapy;
 KW immunoregulatory; antitumour agent; chemotherapy; leukopaenia;
 KW thrombocytopaenia; immunocompetent cell; asthma; hayfever;
 KW rheumatism; interleukin; killer cell.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 73
 FT /label= Ile, Thr
 XX
 PN EP767178-A1.
 XX
 PD 09-APR-1997.
 XX
 PF 26-SEP-1996; 96EP-0306997.

XX 20-SEP-1996; 96JP-0269105.
 PR 26-SEP-1995; 95JP-0270725.
 PR 29-FEB-1996; 96JP-0067434.
 XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 PI Akita K, Fujii M, Kurimoto M, Nukada Y, Tanimoto T;
 XX WPI; 1997-205381/19.
 XX Human protein that induces interferon-gamma prodn. in
 PT immuno:competent cells - useful for adoptive immuno:therapy of
 PT tumours and as antimicrobial agent etc.
 XX Claim 8; Page 20; 26pp; English.
 XX The present sequence represents a novel protein from human cells, which
 CC induces interferon-gamma (IFN gamma) production in immunocompetent cells.
 CC This protein enhances cytotoxicity of killer cells and induces their
 CC formation. It is used as an antineoplastic agent for antitumour
 CC immunotherapy. an antiviral (including anti-AIDS) or antibacterial agent,
 CC and in the treatment of atopic or immune system diseases, e.g. asthma,
 CC hayfever or rheumatism. When formulated with interleukin-3, it is also
 CC used to treat leukaemia and thrombocytopaenia associated with
 CC radiotherapy or chemotherapy of leukaemia and other cancers. When used in
 CC antitumour immunotherapy, this novel protein significantly improves the
 CC immunotherapeutic effect of interleukin-2 (IL-2), compared with use of
 CC IL-2 alone, either when administered to the patient (before
 CC administration of IL-2) or by addition to the medium in which cells
 CC (intended for return to the patient) are being grown.
 XX Sequence 157 AA;
 SQ
 Query Match 99.4%; Score 810; DB 18; Length 157;
 Best Local Similarity 99.4%; Pred. No. 8.1e-83;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
 DB 1 Yfgklesklsvirnlndqvlfidqgnrpfldmtsdcrdnaprtifiismvkdsqprgm 60
 QY 61 AVTISVKCEKISLSCENKIISFKENPPDNIKDTSKDIFFQRSVPGHDNKMQFESSY 120
 DB 61 avtiskcekisxlscenkliisfkennppdnikdtskdiiffqrsvpghdnkmqfessy 120
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
 DB 121 egyflacekerdlfkilkkedelgdrsifmftvqned 157
 RESULT 4
 AAW24258
 ID AAW24258 standard; Protein; 157 AA.
 XX AAW24258;
 XX 15-OCT-1997 (first entry)
 DT Human protein for induction of interferon-gamma.
 DE Interferon-gamma; immunocompetent cell; malignant tumour;
 KW viral disease; bacterial infection; immune disease.
 XX Homo sapiens.
 OS Key Location/Qualifiers
 FH Misc-difference 73
 FT /note= "Encoded by AYT"
 XX JP09157180-A.

PD 17-JUN-1997.
 XX 24-JAN-1996; 96JP-0028722.
 XX 04-OCT-1995; 95JP-0279906.
 PR 10-MAR-1995; 95JP-0078357.
 PR 29-SEP-1995; 95JP-0274988.
 XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 PA WPI; 1997-369391/34.
 DR N-PSDB; AAT80209.
 XX A drug containing a polypeptide which induces interferon-gamma -
 PT useful for treating e.g. malignant tumours, viral, bacterial or
 PT immune diseases
 XX Claim 1; Page 9; 12pp; Japanese.
 PS This sequence represents a protein which induces Interferon-gamma
 CC production in immunocompetent cells. This protein may be used as
 CC the major component in a drug for the prevention and treatment of
 CC e.g. malignant tumours, viral diseases, bacterial infections and
 CC immune diseases.
 XX Sequence 157 AA;
 SQ
 Query Match 99.4%; Score 810; DB 18; Length 157;
 Best Local Similarity 99.4%; Pred. No. 8.1e-83;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
 DB 1 Yfgklesklsvirnlndqvlfidqgnrpfldmtsdcrdnaprtifiismvkdsqprgm 60
 QY 61 AVTISVKCEKISLSCENKIISFKENPPDNIKDTSKDIFFQRSVPGHDNKMQFESSY 120
 DB 61 avtiskcekisxlscenkliisfkennppdnikdtskdiiffqrsvpghdnkmqfessy 120
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
 DB 121 egyflacekerdlfkilkkedelgdrsifmftvqned 157
 RESULT 5
 AAW77158
 ID AAW77158 standard; Protein; 157 AA.
 XX AAW77158;
 XX 26-NOV-1998 (first entry)
 DT Human interleukin-18 protein (IL-18).
 DE Human; interleukin-18 receptor; IL-18R; cytokine; signal transduction;
 KW immune system; treatment; autoimmune; allergic disease;
 KW immunosuppressant.
 XX Homo sapiens.
 OS Key Location/Qualifiers
 FH Misc-difference 73
 FT /note= "Ile or Thr"
 XX EP864585-A1.
 PD 16-SEP-1998.
 XX 23-DEC-1997; 97EP-0310517.
 PR 09-OCT-1997; 97JP-0291837.
 PR 12-MAR-1997; 97JP-0074697.

```

PR 28-JUL-1997; 97JP-0215488.
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX Kurimoto M, Okura T, Torigoe K;
XX
XX WPI; 1998-469188/41.
XX
XX Interleukin-18 receptor polypeptide(s) - and corresponding DNA,
XX which peptide compounds are useful for treating auto-immune or
XX allergic diseases
XX
XX Disclosure: Pages 41-42; 51pp; English.
XX
XX The present sequence represents a human interleukin-18 (IL-18)
XX polypeptide. Interleukin-18 is a type of cytokine which mediates signal
XX transduction in immune systems. The interleukin-18 receptor polypeptide
XX can be used to neutralise interleukin-18 activity or to treat
XX Interleukin-18 receptor susceptible diseases, especially to treat
XX auto-immune or allergic diseases or as an immunosuppressant. Conditions
XX which may be treated include e.g. graft or organ rejection, pernicious
XX anaemia, insulin-related diabetes, discoid lupus erythematosus,
XX ulcerative colitis, hyperthyroidism, auto-immune hepatitis, systemic
XX scleroderma, polymyositis, leukopenia, rheumatoid arthritis, HIV
XX infections, asthma, atopic dermatitis, and pollinosis. The products may
XX also be useful in the treatment of septic shock associated with
XX IFN-alpha.
XX
XX Sequence 157 AA;
SQ

```

Query Match 99.4%; Score 810; DB 19; Length 157;
Best Local Similarity 99.4%; Pred. No. 8.1e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIISMYSKDSQPRGM 60
DB 1 yfgklesklsvirnlndqvlfidqgnrplfedmtsdscrdnprtifiismyskdsqprgm 60
QY 61 AVTISVCKEIKSILSCENKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 120
DB 61 avtisvckekisilscenkiisfkemnpdpdnikdtkdsdiiffqforsvpgdhdkmqfessy 120
QY 121 EGYFLACEKERDLFKLILKKDELDGDRSIMFTVQNE 157
DB 121 egyflacekerdlfklilkkedelgdrsimftvqned 157

```

RESULT 6
AAW77077
ID AAW77077 standard; peptide; 157 AA.
XX
XX AAW77077;
XX
XX 16-NOV-1998 (first entry)
XX
XX Human interleukin 18.
XX
XX Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
XX osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
XX chronic rheumatoid arthritis; deformity ostitis; primary hyperthyroidism.
XX
XX Homo sapiens.
XX
XX EP861663-A2.
XX
XX 02-SEP-1998.
XX
XX 24-FEB-1998; 98EP-0301352.
XX
XX 25-FEB-1997; 97JP-0055468.
XX
XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

```

XX Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;
XX
XX WPI; 1998-448964/39.
XX N-PSDB; AAV48226.
XX
XX Use of interleukin-18 to inhibit osteoclast formation - in treatment
XX of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
XX osteosarcoma, chronic rheumatoid arthritis, deformity ostitis,
XX primary hyperthyroidism and osteoporosis
XX
XX Claim 4; Page 18; 56pp; English.
XX
XX Interleukin-18 (IL-18) or a functional equivalent can be used for
XX inhibition of osteoclast formation. IL-18 is used for treating or
XX preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
XX Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
XX arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and
XX osteoporosis.
XX
XX Sequence 157 AA;
SQ

```

Query Match 99.4%; Score 810; DB 19; Length 157;
Best Local Similarity 99.4%; Pred. No. 8.1e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIISMYSKDSQPRGM 60
DB 1 yfgklesklsvirnlndqvlfidqgnrplfedmtsdscrdnprtifiismyskdsqprgm 60
QY 61 AVTISVCKEIKSILSCENKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 120
DB 61 avtisvckekisilscenkiisfkemnpdpdnikdtkdsdiiffqforsvpgdhdkmqfessy 120
QY 121 EGYFLACEKERDLFKLILKKDELDGDRSIMFTVQNE 157
DB 121 egyflacekerdlfklilkkedelgdrsimftvqned 157

```

RESULT 7
AAW63810
ID AAW63810 standard; protein; 157 AA.
XX
XX AAW63810;
XX
XX 28-SEP-1998 (first entry)
XX
XX Human IL-18 protein fragment.
XX
XX Interleukin-18; IL-18; human; treatment; autoimmune disease; antibody;
XX immunosuppressant; inhibitor; receptor protein; detection.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Protein 1..157
XX /label= IL-18
XX /note= "partial sequence"
XX Misc-difference 73
XX /label= Thr or Ile
XX
XX EP850952-A1.
XX
XX 01-JUL-1998.
XX
XX 23-DEC-1997; 97EP-0310555.
XX
XX 28-JUL-1997; 97JP-0215490.
XX 26-DEC-1996; 96JP-0356426.
XX 21-FEB-1997; 97JP-0052526.
XX 06-JUN-1997; 97JP-0163490.
XX

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PI Kunikata T, Kurimoto M, Torigoe K, Ushio S;
XX WPI: 1998-335317/30.
XX New interleukin-18 receptor protein used to inhibit Interleukin-18,
PT to treat autoimmune disease and as immunosuppressant - and new
PT monoclonal antibody and hybridoma used to detect Interleukin -18
PT receptor protein
XX Claim 5; Page 16; 35pp; English.
XX This sequence represents a human interleukin-18 (IL-18) fragment which is
CC used in a method involved in neutralising IL-18 or to treat autoimmune
CC diseases or as an immunosuppressant using anti-IL-18 antibodies which
CC can inhibit IL-18. Such antibodies can also be used to detect the IL-18
CC receptor protein (labelled with an enzyme or a radioactive or fluorescent
CC substance). The protein is used to treat e.g. graft rejection, pernicious
CC anaemia, atrophic gastritis, insulin-resistant diabetes, Wegener
CC granulomatosis, discoid lupus erythematosus, ulcerative colitis,
CC cold-agglutinin-relating diseases, Goodpasture's syndrome, primary
CC biliary cirrhosis, sympathetic ophthalmitis, hyperthyroidism, juvenile
CC onset type diabetes, Sjogren syndrome, autoimmune hepatitis, autoimmune
CC haemolytic anaemia, myasthenia gravis, systemic scleroderma, systemic
CC lupus erythematosus, polyplectic cold haemoglobinuria, polymyositis,
CC periarthritis nodosa, multiple sclerosis, Addison's disease, purpura
CC haemorrhagica, Basedow's disease, leukopenia, Behcet's disease,
CC Chlamydiae praecox, rheumatoid arthritis, rheumatopyria, chronic
CC thyroiditis, Hodgkin's disease, HIV, asthma, atopic dermatitis, allergic
CC nasitis, pollinosis, apitoxin-allergy and septic shock resulting from
CC production or administration of excessive gamma interferon (IFN-gamma).
XX Sequence 157 AA;

Query Match 99.4%; Score 810; DB 19; Length 157;
Best Local Similarity 99.4%; Pred. No. 8.1e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60
DB 1 Yfgklesklsvirnlndqvlfidqgnrpifedmtsdcrdnaprtfiismykdsqprgm 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDKSDIIFQORSVPGHDKMKQFESSY 120
DB 61 avtisvkcekisxlscenkliisfkemppdnikdktsdiiffqrsvpgdhnmqmfessy 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 121 egyflacekerdlfkilkkedelgdrsImftvqned 157

RESULT 8
AAW37741
ID AAW37741 standard; Protein; 157 AA.
XX AAW37741;
XX AAW37741;
XX 07-JUL-1998 (first entry)
XX IFN-gamma inducing active protein.
XX Interferon-gamma inducing precursor peptide; IFN-gamma;
KW Interleukin-1-beta-converting enzyme; ICE; cytotoxicity; killer cell;
KW antiviral agent; antitumor agent; immunopathy agent; antiseptic.
XX Mammalia.
XX Key Location/Qualifiers
FT Misc-difference 73
FT /label= Ile, Thr
XX

PN EP821005-A2.
XX 28-JAN-1998.
XX 18-JUL-1997; 97EP-0305376.
XX 31-JAN-1997; 97JP-0031474.
PR 25-JUL-1996; 96JP-0213267.
XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX Kurimoto M, Tanimoto T;
XX WPI: 1998-088847/09.
DR N-PSDB; AAV18906.
XX Conversion of interferon-inducing polypeptide precursor to active
PT polypeptide - comprises use of interferon-1-beta-converting enzyme,
PT useful for, e.g. enhancing cytotoxicity by killer cells
XX Claim 5; Page 15; 18pp; English.
XX This is the amino acid sequence for the interferon-gamma (IFN-gamma)
CC inducing active protein which is cleaved to form the active mature
CC protein when it is in contact with interleukin-1-beta-converting
CC enzyme (ICE). The polypeptide is used for inducing, e.g. production
CC of IFN-gamma a useful biologically active substance, enhancing
CC cytotoxicity by, and inducing the formation of killer cells. The
CC polypeptide may potentially be used as an antiviral, antitumour and
CC immunopathy agent and as an antiseptic.
XX Sequence 157 AA;

Query Match 99.4%; Score 810; DB 19; Length 157;
Best Local Similarity 99.4%; Pred. No. 8.1e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60
DB 1 Yfgklesklsvirnlndqvlfidqgnrpifedmtsdcrdnaprtfiismykdsqprgm 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDKSDIIFQORSVPGHDKMKQFESSY 120
DB 61 avtisvkcekisxlscenkliisfkemppdnikdktsdiiffqrsvpgdhnmqmfessy 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 121 egyflacekerdlfkilkkedelgdrsImftvqned 157

RESULT 9
AAW52176
ID AAW52176 standard; peptide; 157 AA.
XX AAW52176;
XX AAW52176;
XX 10-JUN-1998 (first entry)
XX Interferon-gamma inducing mature polypeptide.
XX Interferon-gamma; IFN-gamma; precursor; enzyme; cleavage.
XX Homo sapiens.
XX Key Location/Qualifiers
FT Misc-difference 73
FT /label= Ile, Thr
XX EP819757-A2.
XX 21-JAN-1998.
XX

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PF 18-JUL-1997; 97EP-0305377.
XX
PR 30-MAY-1997; 97JP-0156062.
PR 19-JUL-1996; 96JP-0207691.
XX
FA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Kurimoto M, Tanimoto T;
XX
DR WPI; 1998-078838/08.
XX
PT Polypeptide-processing enzyme - for preparing mature form of
PT interferon-inducing polypeptide
XX
PS Claim 20; Page 17; 18pp; English.
XX
CC This is an Interferon-gamma (IFN-gamma) inducing polypeptide sequence.
CC This polypeptide induces IFN-gamma production in immunocompetent cells
CC [the polypeptide is not named but is described in JP 27198/96 and
CC 193098/96]. An enzyme can convert the precursor form of this polypeptide
CC into this active form by cleaving a linkage between Asp at amino acid
CC position 36 and Tyr at amino acid position 37 of the precursor. The
CC enzyme can be obtained from a human haematopoietic cell and can be
CC inhibited by iodoacetamide and acetyl-L-tyrosyl-L-valyl-L-alanyl-L-
CC aspartyl-L-al. The enzyme can be used for cleaving a recombinant IFN-gamma
CC pro-polypeptide to form a mature polypeptide.
XX
SQ Sequence 157 AA;

Query Match 99.4%; Score 810; DB 19; Length 157;
Best Local Similarity 99.4%; Pred. No. 8.le-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60
Db 1 yfgklesklsvirnlndqvlfdggnrplfedmtdsdcdrdnprtifiismykdsqprgm 60

Qy 61 AVTISVKCEKISILSCENKIISFKEMNPPDNIKDTKSDIIFFORSVPGHDNKMOPFESSY 120
Db 61 avtislsvkcekisxlscenkiisfkemppdpndniktdksdiiffqrsvpghdnkmqfessy 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 egyflacekerdlfklikkedelgdrsimftvqned 157

RESULT 10
AAAY39799
ID AAY39799 standard; Protein; 157 AA.
XX
AC AAY39799;
XX
DT 29-NOV-1999 (first entry)
XX
DE Interleukin-18 receptor protein sequence fragment.
XX
KW Interleukin-18 receptor; IL-18; human; mouse; organ transplant rejection;
KW IL-18 receptor sensitive disease; immune reaction; therapy.
XX
OS Mammalia.
XX
FH Key Location/Qualifiers
FT Misc-difference 73 /note= "unspecified amino acid"
XX
PN JPI1240898-A.
XX
PD 07-SEP-1999.
XX
PF 12-MAR-1998; 98JP-0078549.
XX
PR 12-MAR-1997; 97JP-0074697.

28-JUL-1997; 97JP-0215488.
09-OCT-1997; 97JP-0291837.
26-DEC-1997; 97JP-0366908.
XX
FA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
DR WPI; 1999-555071/47.
XX
PT New polypeptide - useful against interleukin-18 receptor sensitive
PT diseases
XX
PS Disclosure; Page 37; 41pp; Japanese.
XX
CC This sequence is a fragment of an interleukin-18 receptor (IL-18R) of the
CC invention. The IL-18R sequences were isolated from human and mouse. The
CC sequences can be used in drugs for treating IL-18 receptor sensitive
CC disease, especially effective for the relief of rejection accompanied to
CC organ transplantation and for the treatment and the prevention of various
CC diseases caused by excessive immune reaction.
XX
SQ Sequence 157 AA;

Query Match 99.4%; Score 810; DB 20; Length 157;
Best Local Similarity 99.4%; Pred. No. 8.le-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60
Db 1 yfgklesklsvirnlndqvlfdggnrplfedmtdsdcdrdnprtifiismykdsqprgm 60

Qy 61 AVTISVKCEKISILSCENKIISFKEMNPPDNIKDTKSDIIFFORSVPGHDNKMOPFESSY 120
Db 61 avtislsvkcekisxlscenkiisfkemppdpndniktdksdiiffqrsvpghdnkmqfessy 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 egyflacekerdlfklikkedelgdrsimftvqned 157

RESULT 11
AAAY44597
ID AAY44597 standard; Protein; 157 AA.
XX
AC AAY44597;
XX
DT 04-APR-2000 (first entry)
XX
DE Human interleukin-18.
XX
KW Human interleukin-18; IL-18; anti-IL-18-antibody; immunopathies;
KW inflammatory disorder; autoimmune disease; anti-allergic;
KW anti-inflammatory; immunosuppressive; hematopoietic; leukocytopoietic;
KW antialgic; antipyretic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 73 /label= Ile, Thr
XX
PN EP974600-A2.
XX
PD 26-JAN-2000.
XX
PF 24-JUN-1999; 99EP-0304977.
XX
PR 24-JUN-1998; 98JP-0177580.
PR 12-OCT-1998; 98JP-0289044.
PR 22-DEC-1998; 98JP-0365023.
XX
FA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX

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```
PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;
XX WPI; 2000-118341/11.
XX
XX New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases -
XX
XX Example 1; Page 26; 32pp; English.
XX
XX The present sequence is human interleukin-18. This was used to immunise
CC BALB/c mice to generate hybridomas that produce anti-IL-18 antibodies for
CC neutralising interleukin-18. This is useful for treating and preventing
CC immunopathies, inflammatory disorders and autoimmune diseases which are
CC caused by excessive immunoreaction. The protein has anti-allergic
CC anti-inflammatory, immunosuppressive, hematopoietic, leukocytopoietic,
CC antiagtic, antipyretic and hepatic-function improving activities.
XX
SQ Sequence 157 AA;
Query Match 99.4%; Score 810; DB 21; Length 157;
Best Local Similarity 99.4%; Pred. No. 8.1e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDSCRDNAPRTIFISMYKDSQPRGM 60
Db 1 Yfgklesklsvirnlndqvlfidqgnrplfedmtsdscrdnprtfiflismykdsqprgm 60
Qy 61 AVTISVKEKISILSCENKIISFKEMNPPDNIKDKTSIIFFQRSVPGHDKNMQFESSY 120
Db 61 avtisvkekisxlscenkiisfkemppdnikdktsdiiffqrsvpghdnkmqfessy 120
Qy 121 EGYFLACEKERDLFLILKKEDELGDRSIMFTVQNEQ 157
Db 121 egyflacekerdlflkllkkedelgdrsimftvqned 157
RESULT 12
AAV53904
ID AAV53904 standard; Protein: 157 AA.
AC AAV53904;
DT 13-MAR-2000 (first entry)
DE Sequence of a mature protein that induces IFN-gamma production.
XX
KW Human; interferon gamma production; IFN-gamma; immunocompetent cell;
KW antiviral; immunoregulatory; antigen; mitogen;
KW IFN-gamma susceptible disease; antibacterial; antitumour;
KW blood platelet enhancing agent; hepatitis; herpes syndrome; condyloma;
KW AIDS; bacterial disease; candidiasis; malaria; solid malignant tumour;
KW renal cancer; mycosis fungoides; chronic granulomatous disease;
KW blood cell malignant tumour; adult T cell leukaemia;
KW chronic myelogenous leukaemia; malignant leukaemia; immune disease;
KW allergy; rheumatism.
XX
OS Homo sapiens.
FH
FH Key Location/Qualifiers
FT Misc-difference 73
FT /label= Ile, Thr
FT /note= "encoded by AVT"
XX
PN EP962531-A2.
XX
XX 08-DEC-1999.
XX
XX 10-NOV-1995; 99EP-0104104.
XX
XX 15-NOV-1994; 94JP-0304203.
PR 23-FEB-1995; 95JP-0058240.
PR
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PR 10-MAR-1995; 95JP-0078357.
PR 18-SEP-1995; 95JP-0262062.
PR 29-SEP-1995; 95JP-0274988.
PR 10-NOV-1995; 95EP-0308055.
XX
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
PA
XX Ushio S, Torigoe K, Tanimoto T, Okamura H;
XX
XX WPI; 2000-064289/06.
DR N-PSDB; AAZ36875.
XX
XX Novel polypeptides used in the treatment of Interferon-gamma
PT susceptible diseases -
XX
XX Claim 1; Page 4; 42pp; English.
XX
XX The present sequence represnets a human protein that induces Interferon
CC (IFN)-gamma production by immunocompetent cells. IFN-gamma is a
CC protein which has antiviral, antioncotic and immunoregulatory activities,
CC and is produced by immunocompetent cells stimulated with antigens or
CC mitogens. The protein of the invention is used to treat IFN-gamma
CC susceptible diseases, and also have use as a antiviral agent,
CC antibacterial agent, antitumour agent, immunoregulatory agent and blood
CC platelet enhancing agent. Diseases which can be treated with the
CC protein include viral diseases such as hepatitis, herpes syndrome,
CC condyloma, and AIDS; bacterial diseases such as candidiasis and
CC malaria; solid malignant tumours such as renal cancer, mycosis
CC fungoides, and chronic granulomatous disease; blood cell malignant
CC tumours such as adult T cell leukaemia, chronic myelogenous leukaemia,
CC and malignant leukaemia; and immune diseases such as allergy and
CC rheumatism.
XX
SQ Sequence 157 AA;
Query Match 99.4%; Score 810; DB 21; Length 157;
Best Local Similarity 99.4%; Pred. No. 8.1e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDSCRDNAPRTIFISMYKDSQPRGM 60
Db 1 Yfgklesklsvirnlndqvlfidqgnrplfedmtsdscrdnprtfiflismykdsqprgm 60
Qy 61 AVTISVKEKISILSCENKIISFKEMNPPDNIKDKTSIIFFQRSVPGHDKNMQFESSY 120
Db 61 avtisvkekisxlscenkiisfkemppdnikdktsdiiffqrsvpghdnkmqfessy 120
Qy 121 EGYFLACEKERDLFLILKKEDELGDRSIMFTVQNEQ 157
Db 121 egyflacekerdlflkllkkedelgdrsimftvqned 157
RESULT 13
AAV57570
ID AAV57570 standard; protein; 157 AA.
XX
XX AAV57570;
AC
XX
XX 06-MAR-2000 (first entry)
DT
DE Human interleukin 18 protein sequence SEQ ID NO:1.
XX
XX Human; interleukin 18; IL-18; potentlator; IGIF;tumour; cancer;
KW interferon-gamma-inducing factor; growth inhibition; cytostatic.
XX
XX Homo sapiens.
XX
XX WO9959565-A1.
XX
XX 25-NOV-1999.
XX
XX 20-MAY-1999; 99WO-US11160.
PF
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 8, 2002, 10:12:19 ; Search time 28.21 Seconds
(without alignments)
534.776 Million cell updates/sec

Title: SEQ6ILEAT73
Perfect score: 815
Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKDELGDRSIMFTVQNE 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	514	63.1	192	2 S60226	cytokine IGIF - mouse
2	84	10.3	381	2 T40341	hypothetical prote
3	84	10.3	452	2 D64583	hypothetical prote
4	83.5	10.2	270	1 S10532	interleukin-1 alph
5	83.5	10.2	866	2 C71509	probable DNA polym
6	82	10.1	263	2 T39487	hypothetical prote
7	82	10.1	364	2 A81261	probable periplasm
8	79	9.7	632	2 T00679	hypothetical prote
9	78.5	9.6	192	2 S15661	(2'-5')oligo(A) sy
10	78	9.6	473	2 T32038	hypothetical prote.
11	77.5	9.5	270	2 I46620	interleukin-1 alph
12	77.5	9.5	1228	2 A57384	multimerin, endoth
13	76.5	9.4	204	2 T44357	hypothetical prote
14	76.5	9.4	1036	2 H64245	hypothetical prote
15	76	9.3	450	2 G71928	hypothetical prote
16	76	9.3	747	2 E84698	hypothetical prote
17	75.5	9.3	1251	2 A56677	neuronal cell cycl
18	75	9.2	354	2 E97128	magnesium and ciba
19	75	9.2	1738	2 T14867	intrapatin - slime
20	75	9.2	2663	1 S28261	centromere protein
21	74.5	9.1	268	1 B24073	interleukin-1 alph
22	74.5	9.1	334	2 T04198	hypothetical prote
23	74.5	9.1	888	2 A38539	pi01 protein precu
24	74.5	9.1	1663	1 C3MS	complement C3 prec
25	74	9.1	245	2 B90488	hypothetical prote
26	74	9.1	376	2 T24925	hypothetical prote
27	74	9.1	1064	1 S57450	protein-tyrosine k
28	74	9.1	2470	2 I50726	cation-independent
29	73.5	9.0	375	2 T29568	hypothetical prote

30	73.5	9.0	475	2 T32036	hypothetical prote
31	73.5	9.0	728	2 T24716	hypothetical prote
32	73.5	9.0	871	2 T48502	hypothetical prote
33	73.5	9.0	1246	2 S60954	probable membrane
34	73	9.0	467	2 A47388	serine/threonine p
35	73	9.0	680	2 A28121	major merozoite su
36	73	9.0	810	2 B71639	virb4 protein prec
37	73	9.0	1772	2 A45532	major merozoite su
38	72.5	8.9	436	2 G97701	polynucleotide ade
39	72.5	8.9	467	2 A48713	serine/threonine-s
40	72.5	8.9	527	2 S42512	recombination-acti
41	72.5	8.9	586	2 C70091	conserved hypothet
42	72.5	8.9	1510	2 T16927	hypothetical prote
43	72	8.8	264	2 B90051	hypothetical prote
44	72	8.8	361	2 E96904	minD family ATPase
45	72	8.8	440	2 F70117	hypothetical prote

ALIGNMENTS

RESULT 1

S60226
cytokine IGIF - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C:Accession: S60226
R:Okamura, H.; Tsutsui, H.; Komatsu, T.; Yutsudo, M.; Hakura, A.; Tanimoto, T.; Torig

Nature 378, 88-91, 1995

A:Title: Cloning of a new cytokine that induces IFN-gamma production by T cells.
A:Reference number: S60226; MUID:96061009
A:Accession: S60226
A:Status: preliminary
A:Molecule type: mrna
A:Residues: 1-192 <OKA>
A:Cross-references: EMBL:D49949; NID:g1064822; PIDN:BAA08705.1; PID:g1064823
C:Superfamily: Mus musculus cytokine IGIF

Query Match 63.1%; Score 514; DB 2; Length 192;

Best Local Similarity 64.9%; Pred. No. 2.4e-41;

Matches 100; Conservative 27; Mismatches 25; Indels 2; Gaps 2;

Qy 2 FGLKLESKLSVIRNLNDQVLFDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGMA 61

Db 37 FGLRHCTTAVIRNLNDQVLFDVK-RQPVFEDMTDIDQSASEPQTRLIIIMYKDSVRLGA 95

Qy 62 VTISVKCEKISILSCENKIIISFKEMNPPDNIKDKSDIIFQORSVPGHDNKMQFESSSVE 121

Db 96 VTLSVKDSKMSLTSCNKKIISFEEMDPENIDDDIQTSDLIFFQKRVPGH-NKMEFESSLYE 154

Qy 122 GYFLACERDLFKLILKKEDELGDRSIMFTVQN 155

Db 155 GHFLACQKREDAFLKILKKEDEGSKSVMTLTN 188

RESULT 2

T40341

hypothetical protein SPBC3B9.02c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T40341
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, March 1997
A:Reference number: 221922

A:Accession: T40341

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-381 <WOO>

A:Cross-references: EMBL:AL022070; PIDN:CAA17782.1; GSPDB:GN00067; SPDB:SPBC3B9.02c

A:Experimental source: strain 972h-; cosmid c3B9

C:Genetics:

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
C:Accession: T39487
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lucas, M.; Gaillardin, C.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z21858
A:Accession: T39487
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-263 <LVN>
A:Cross-references: EMBL:AL031349; PIDN:CAA20486.2; GSPDB:GN00067; SPDB:SPBC15D4.11c
A:Experimental source: strain 972h; cosmid c15D4
C:Genetics:
A:Gene: SPDB:SPBC15D4.11c
A:Map position: 2
A:Introns: 96/2; 147/3
C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC15D4.11c

Query Match 10.1%; Score 82; DB 2; Length 263;
Best Local Similarity 21.7%; Pred. No. 2.6;
Matches 35; Conservative 33; Mismatches 65; Indels 28; Gaps 5;

QY 4 KLESLVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRIFIISMVKDSQPRGMATV 63

DB 47 KLDSELGVYKQVLDLTPKKGYEKALHSFIHED-----PSLVNISALKETAKIRVT 100

QY 64 ISVKCEKISLSCENKIISFKEMNPDPNIDKTSIDIFQORSVPGH----- 109

DB 101 VPVYSRSKYV--QYKPIHSAEN--ENGNETSDELVFQHSIPAKVQLTNHNGTILCAL 156

QY 110 ---DNKMQFESSYEGYFLACEKERDLFKLILKKEDELGDR 147

DB 157 ILCKGMLHFDSTISFQSPQNSQAFSSDL-RLILQKSKQYTR 196

RESULT 7

A:1261

probable periplasmic protein Cj1643 [imported] - Campylobacter jejuni (strain NCTC 11168)

C:Species: Campylobacter jejuni

C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000

C:Accession: A81261

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barre

Nature 403, 665-668, 2000

A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp

A:Reference number: A81250; MUID:20150912

A:Accession: A81261

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-364 <PAR>

A:Cross-references: GB:AL139079; GB:AL111168; NID:g6968971; PIDN:CAB73631.1; PID:g696906

A:Experimental source: serotype O2, strain NCTC 11168

C:Genetics:
A:Gene: Cj1643

Query Match 10.1%; Score 82; DB 2; Length 364;

Best Local Similarity 25.5%; Pred. No. 3.8;

Matches 39; Conservative 21; Mismatches 39; Indels 54; Gaps 9;

QY 12 IRLNDQVLFIDQGNRPLFEDMTSDCRD-NAPRIFIISMVK-----DSQPR----- 58

DB 211 LRKLEKILFADRGSTLYFQVLRDN--MDLNISTEVFAKDLKSNLPDSKPKKITNFTS 268

QY 59 --GMAVTISVKCEKI-----SILSENKII-SFKEMNPDPNI----- 92

DB 269 NLGLTVNASLVVTKIDPKSKSVNAGFMVGDKILRVNNIILNFKEL---QNILSAGNDPS 325

QY 93 -----KDTKSDIIFQORSVPGH-----DNKMQF 115

DB 326 ILIERKSTKLPLSNFENNEJLGGNAGSGDGKQF 358

RESULT 8

T00679

hypothetical protein At2g43990 [imported] - Arabidopsis thaliana

N:Alternate names: hypothetical protein F6E13.12

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001

C:Accession: T00679; A84873

R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Syke

submitted to the EMBL Data Library, June 1998

A:Description: Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence.

A:Reference number: Z14180

A:Accession: T00679

A:Status: translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-632 <ROU>

A:Cross-references: EMBL:AC004005; NID:g3212846; PID:g3212856

A:Experimental source: cultivar Columbia

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Water

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana

A:Reference number: A84420; MUID:20083487

A:Accession: A84873

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-632 <STO>

A:Cross-references: GB:AE002093; NID:g3212856; PIDN:AAC23407.1; GSPDB:GN00139

C:Genetics:
A:Gene: At2g43990; F6E13.12

A:Map position: 2

Query Match 9.7%; Score 79; DB 2; Length 632;

Best Local Similarity 25.6%; Pred. No. 14;

Matches 34; Conservative 30; Mismatches 39; Indels 30; Gaps 9;

QY 28 PLFDWTDSD-CRDNAPRIFIISMVKDSQPRGMATVTSVKCEK-----ISILSCENK 79

DB 368 PLSDRSASSDLNCSGRSLSPMDIYKETRR---ISSLSLSPNEILFRFRFTHLSSCDGE 424

QY 80 IISFK-----EMPNPDNIDKTSIDIFFORSVP--GHDNKMQF--ESSSYEGYF-LACBK 129

DB 425 ASAFDTSPTCELDPSHLKDGKSSPL---SVDTLGSENVITPESNSSFDNVFGLSCSQ 480

QY 130 ERDLFKLILKKED 142

DB 481 AE-----IQKKHD 488

RESULT 9

S15661

(2'-5')oligo(A) synthetase (EC 2.7.7.-) L1 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #text_change 16-Jul-1999

C:Accession: S15661; S19108

R:Rutherford, M.N.; Kumar, A.; Nissim, A.; Chebath, J.; Williams, B.R.G.

Nucleic Acids Res. 19, 1917-1924, 1991

A:Title: The murine 2-5A synthetase locus: three distinct transcripts from two linked

A:Reference number: S15660; MUID:91232962

A:Accession: S15661

A:Molecule type: mRNA

A:Residues: 1-192 <RUT>

A:Cross-references: EMBL:X55982

R:Williams, B.
submitted to the EMBL Data Library, September 1990

A:Reference number: S19108

A:Accession: S19108

A:Molecule type: mRNA

A:Residues: 1-175, 'L', 177-192 <WIL>

A:Cross-references: EMBL:X55982; NID:g49714; PIDN:CAA39455.1; PID:g49715

C:Superfamily: oligo(A) synthetase

C:Keywords: nucleotidyltransferase

RESULT 13
T44357
hypothetical protein [Imported] - Clostridium histolyticum
C:Species: Clostridium histolyticum
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T44357
R:Ratsushita, O.; Jung, C.M.; Katayama, S.; Minami, J.; Takahashi, Y.; Okabe, A.
J. Bacteriol. 181, 923-933, 1999
A:Title: Gene duplication and multiplicity of collagenases in Clostridium histolyticum.
A:Reference number: 222752; MUID:99121032
A:Accession: T44357
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-204 <NAT>
A:Cross-references: EMBL:AB014075; NID:g3868863; PIDN:BAA3454.1; PID:g3892648
A:Experimental source: strain JCM 1403

Query Match	9.4%	Score	76.5	DB 2	Length	204			
Best Local Similarity	26.4%	Pred. No.	6.3						
Matches	32	Conservative	19	Mismatches	51	Indels	19	Gaps	5

QY 9 LSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFII--SMYKDSQPRGMAVTISV 66

25 1STEENBNHKA SSNKOCEAKTCETN-----TDCNSENCTIVUESVIV KDCCEANWTWIDE 80

QY	67	KCEK-----ISILSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKMOfESS	119
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01 07 08 09 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 10

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RESULT 14

H64245
hypothetical protein MG414 - Mycoplasma genitalium
C:Species: Mycoplasma genitalium
C:date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 02-Mar-2001
C:Accession: H64245; G64245
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
, C.A.; Venter, J.C.
Science 270, 397-403, 1995
A:title: The minimal gene complement of Mycoplasma genitalium.

Query Match	9.4%	Score 76.5;	DB 2;	Length 1036;
Best Local Similarity	21.9%	Pred. No. 43;		
Matches 33;	Conservative	33;	Mismatches	64;
			Indels	21;
			Gaps	6;

Qy 14 NLNDQVLFIDQGNRPLFED--MTDSDCRDNAPRTIFIISMYKDSQPRGMAVTISVKCEKI 71

845 SI NDEFOI I VOKAI NTITI SEKROI OTTAKANUPENI VNAKPTINTUJ VEMIAKOCNI VEMIAKOCNI VEMIAKOCNI 004

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 8, 2002, 10:13:54 ; Search time 15.78 Seconds
(without alignments)
385.233 Million cell updates/sec

Title: SEQ6ILEAT73

Perfect score: 815

Sequence: 1 YFGKLESKLSVIRNLDQVL.....LKKEDLGDRSINFTVQNE 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	DB	ID	Description
1	810	99.4	193	1	IL18_HUMAN	Q14116 homo sapien
2	658	80.7	193	1	IL18_HORSE	Q9XSG7 equus cabal
3	653	80.1	193	1	IL18_BOVIN	Q9TU73 bos taurus
4	636	78.0	192	1	IL18_PIG	Q19073 sus scrofa
5	612	75.1	193	1	IL18_CANEA	Q9XSR0 canis famil
6	514	63.1	192	1	IL18_MOUSE	P70380 mus musculu
7	513.5	63.0	194	1	IL18_RAT	P97636 rattus norv
8	83.5	10.2	270	1	IL1A_PIG	P18430 sus scrofa
9	83	10.2	267	1	IL1A_RABIT	P04822 oryctolagus
10	78.5	9.6	192	1	OSAB_MOUSE	Q60856 mus musculu
11	77.5	9.5	270	1	IL1A_HORSE	Q28385 equus cabal
12	77.5	9.5	1228	1	ECM_HUMAN	Q13201 homo sapien
13	76.5	9.4	527	1	RAG2_HUMAN	P53895 homo sapien
14	76.5	9.4	1036	1	Y414_MYCGE	P47653 mycoplasma
15	75	9.2	2663	1	CENE_HUMAN	Q02224 homo sapien
16	74.5	9.1	1663	1	C03_MOUSE	P01027 mus musculu
17	74	9.1	270	1	IL1A_FELCA	O46613 felis silve
18	74	9.1	426	1	YXCC_ASTLO	P58151 astasia lon
19	73.5	9.0	375	1	YIC5_CAEEL	Q18610 caenorhabdi
20	73	9.0	467	1	M3K8_RAT	Q63562 rattus norv
21	73	9.0	1772	1	MSPI_PLAYO	P13828 plasmodium
22	72.5	8.9	527	1	RAG2_RABIT	P34089 oryctolagus
23	72	8.8	467	1	M3K8_MOUSE	Q07174 mus musculu
24	71.5	8.8	691	1	Y104_YEAST	P40460 saccharomyc
25	70.5	8.7	313	1	COL4_ARATH	Q9M9B3 arabidopsi
26	70.5	8.7	644	1	YGM4_YEAST	P53129 saccharomyc
27	70.5	8.7	711	1	TRFL_HUMAN	P03788 homo sapien
28	70.5	8.7	853	1	PHS1_DICDI	Q00766 dictyosteli
29	70.5	8.7	1114	1	RH18_YEAST	Q12749 saccharomyc
30	70	8.6	253	1	ADLY_ECOLI	P33234 escherichia
31	70	8.6	700	1	NONA_DROME	Q04047 drosophila
32	70	8.6	1481	1	CFTR_BOVIN	P35071 bos taurus
33	70	8.6	2273	1	ABCR_HUMAN	P78363 homo sapien

34	70	8.6	3317	1	CADN_RAT	P58365 rattus norv
35	70	8.6	3354	1	CADN_MOUSE	Q99GF4 mus musculu
36	70	8.6	4590	1	FATH_HUMAN	Q14517 homo sapien
37	69.5	8.5	268	1	IL1A_BOVIN	P08831 bos taurus
38	69.5	8.5	467	1	M3K8_HUMAN	P41279 homo sapien
39	69.5	8.5	875	1	POP1_YEAST	P41812 saccharomyc
40	69.5	8.5	1830	1	BP28_ARATH	Q9C8Z4 arabidopsi
41	69	8.5	269	1	MBKE_KLEPN	P21649 klebsiella
42	69	8.5	578	1	TRML_DROME	Q9VK89 drosophila
43	69	8.5	586	1	SYD_BORBU	O51402 borrelia bu
44	68.5	8.4	268	1	IL1A_CAPHI	P79161 capra hircu
45	68.5	8.4	270	1	IL1A_MOUSE	P01582 mus musculu

ALIGNMENTS

```
RESULT 1
IL18_HUMAN
ID IL18_HUMAN STANDARD; PRT: 193 AA.
AC Q14116; O75599;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96247646; PubMed=8666798;
RA Ushio S., Namba M., Okura T., Hattori K., Nukada Y., Akita K.,
RA Tanabe F., Konishi K., Micallef M., Fujii M., Torigoe K., Tanimoto T.,
RA Fukuda S., Ikeda M., Okamura H., Kurimoto M.;
RT "Cloning of the cDNA for human IFN-gamma-inducing factor, expression
RT in Escherichia coli, and studies on the biologic activities of the
RT protein.";
RL J. Immunol. 156:4274-4279(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Yong D., Guixin D., Lihua H., Haitao W.;
RT "Cloning and sequencing of the cDNA for precursor hIL-18.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Liu J., Peng X., Yuan J., Qiang B.;
RT "Cloning of human interleukin 18 cDNA.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 2-193 FROM N.A.
RC TISSUE=Peripheal blood;
RA Conti B., Kim S.J., Tinti C., Chun H.S., Joh T.H.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
-!- AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CELLS.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
```

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EMBL; D49950; BAA08706.1; -.
EMBL; AF077611; AAC27787.1; -.

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Best Local Similarity   77.7%;   Pred No. 4.2e-54;
Matches 122; Conservative 21; Mismatches 14; Indels 0; Gaps 0

QY 1 YFGKLESKLIVRNLDVLFIDOGNRLPFLFEDWTDSDCRDNAPRTIFIIISWKDSQPRGM 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 37 YFGRLEPKLSIIRNLNDQVLFINQGNQPVFEDMPDSDCTDNAPTVEFIYYKDSLTRGL 96

QY 61 AVTISVKCEKISILSCENKIISFKEMNPDPNIKDKTSDIFFQRSPVGHDKMKQFESSY 120
    |||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 97 AVTISVKCETSTLSCENKIISFKEMSPPEINDEGNDIIFFQRSPVGHDDKIQFESSLY 156

QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTQNED 157
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 157 KGyFLACEKENDLFKLLKKEDENGDKSVMTFNQON 193

RESULT      3
IL18_BOVIN STANDARD;          PRT;       193 AA.
AC Q9TU73;
AD 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20012648; PubMed=10547157;
RA Shoda L.K., Zarlenga D.S., Hirano A., Brown W.C.;
RT "Cloning of a cDNA encoding bovine interleukin-18 and analysis of IL-
RT 18 expression in macrophages and its IFN-gamma-inducing activity." ;
RL J. Interferon cytokine Res. 19:1169-1177(1999).
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF124789; AAF08686.1; .
CC InterPro; IPR000975; Interleukin_1.
CC SMART; SM00125; IL1; 1.
KW Cytokine.
FT PROPEP             1       36     BY SIMILARITY.
FT CHAIN              37      193   INTERLEUKIN-18.
SEQUENCE 193 AA; 22347 MW; 65720F199DEA49C4 CRC64;

Query Match           80.18; Score 653; DB 1; Length 193;
Best Local Similarity 77.18; Pred. No. 1.2e-53;
Matches 121; Conservative 23; Mismatches 13; Indels 0; Gaps 0

QY 1 YFGKLESKLIVRNLDVLFIDOGNRLPFLFEDWTDSDCRDNAPRTIFIIISWKDSQPRGM 60
    |||:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 37 HFGKLEPKLSIIRNLNDQVLFINQGNQPVFEDMPDSDCS DNAPTVEFIYYKDSLTRGL 96

QY 61 AVTISVKCEKISILSCENKIISFKEMNPDPNIKDKTSDIFFQRSPVGHDKMKQFESSY 120
    |||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 97 AVTISVCKMNSTLSCENKNIVSFKMNPDPNIIDNESDIIFFQRSPVGHDDKIQFESSLY 156
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=96061009; PubMed=7477296;
RA Okamura H., Tsutui H., Komatsu T., Yutsudo M., Hakura A.,
RA Tanimoto T., Torigoe K., Okura T., Nakada Y., Hattori K.,
RA Akita K., Namba M., Tanabe F., Konishi K., Fukuda S., Kurimoto M.;
RT "Cloning of a new cytokine that induces IFN-gamma production by T
RT cells.";
RL Nature 378:88-91(1995).
RN [2]
RP SEQUENCE OF 1-191 FROM N.A.
RC STRAIN=MOD; TISSUE=Pancreas;
RX MEDLINE=97174346; PubMed=9022080;
RA Rothe H., Jenkins N.A., Copeland N.G., Kolb H.;
RT "Active stage of autoimmune diabetes is associated with the
RT expression of a novel cytokine, IGIF, which is located near Idd2.";
RL J. Clin. Invest. 99:469-474(1997).
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
CC -----
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CC -----
DR EMBL; D49949; BAA08705.1; -.
DR EMBL; U66244; AAB49753.1; -.
DR MGD; MGI:107936; IL18.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 35
FT CHAIN 36 192 INTERLEUKIN-18.
FT CONFLICT 183 185 MFT -> IS (IN REF. 2).
FT CONFLICT 183 185 MFT -> IS (IN REF. 2).
SQ SEQUENCE 192 AA; 22135 MW; 8FED938473874D63 CRC64;

Query Match 63.1%; Score 514; DB 1; Length 192;
Best Local Similarity 64.9%; Pred. No. 8.9e-41;
Matches 100; Conservative 27; Mismatches 25; Indels 2; Gaps 2;

QY 2 FGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGMA 61
DB 37 FGLRHCTTAVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGMA 61
QY 62 VTISVKCEKISLSCENKIIISFKEMNPPDNIKDKSIIFFORSVPGHDKMKOFESSYE 121
DB 96 VTLSVKDSKSTLSCKNKIISFEMDPENIDDIQSDLIFFQKRVPGH-NKMEESSLYE 154
QY 122 GYFLACERDLFKILKKEDELGDRSIMFTVQN 155
DB 155 GHFLACQKEDDAFKLILKXKDKENGDKSVMTLTN 188

RESULT 7
IL18_RAT
ID IL18_RAT STANDARD; PRT; 194 AA.
AC P97636; p97637; O88749;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)

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DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Adrenal gland;
RX MEDLINE=97152963; PubMed=8999896;
RA Conti B., Jahng J.W., Tinti C., Son J.H., Joh T.H.;
RT "Induction of interferon-gamma inducing factor in the adrenal
RT cortex.";
RL J. Biol. Chem. 272:2035-2037(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RX MEDLINE=98368130; PubMed=9702748;
RA Culhane A.C., Hall M.D., Rothwell N.J., Luheshi G.N.;
RT "Cloning of rat brain interleukin-18 cDNA.";
RL Mol. Psych. 3:362-366(1998).
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
CC -----
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CC -----
DR EMBL; U77776; AAC53009.1; -.
DR EMBL; U77777; AAC53010.1; -.
DR EMBL; AJ222813; CAAL1001.1; -.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
KW Cytokine; Alternative splicing.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 194 INTERLEUKIN-18.
FT CONFLICT 121 139 MISSING (IN ISOFORM ALPHA).
FT VARSPLIC 4 5 MS -> IP (IN REF. 2).
FT CONFLICT 48 48 I -> M (IN REF. 2).
SQ SEQUENCE 194 AA; 22303 MW; E2089AD6F1798450 CRC64;

Query Match 63.0%; Score 513.5; DB 1; Length 194;
Best Local Similarity 63.2%; Pred. No. 1e-40;
Matches 98; Conservative 28; Mismatches 28; Indels 1; Gaps 1;

QY 1 YFKLESKLVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60
DB 37 HFGRHCTTAVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60
QY 61 AVTSVKCEKISLSCENKIIISFKEMNPPDNIKDKSIIFFORSVPGHDKMKOFESSY 120
DB 97 AVTSLVKDGRMSTLSCKNKIISFEMNPPDNIDDIQSDLIFFQKRVPGH-NKMEFESSLY 155
QY 121 EGYFLACERDLFKILKKEDELGDRSIMFTVQN 155
DB 156 EGFLACQKEDDAFKLILKXKDKENGDKSVMTLTN 190

RESULT 8
IL1A_PIG
ID IL1A_PIG STANDARD; PRT; 270 AA.
AC P18430;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)

```


Db 127 LRIKQEFLLNDALNQSLVRDTSQYLRAAPLQNLGDAVKFDMGVMTSEDSILPVLTRI 186
 QY 67 KCEKISI-LSCENKIIFKEM-NPNDNIKOTKSDIIFQFQSVPCVCHDKNKMOPFESSYEGYF 124
 Db 187 SOTPLFVSAQNEDEPVLKKEMPETPRIITSDSEILFFWET---QGKNKVFKSAAPOLF 243

QY 125 LACEKE 130
 Db 244 IATKPE 249

RESULT 10
 OASB_MOUSE STANDARD; PRT; 192 AA.
 AC Q60856;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 2'-5'-oligoadenylate synthetase 1B (EC 2.7.7.-) ((2-5')oligo(A)
 DE synthetase 1b) (2-5A synthetase 1B) (Fragment).
 GN OAS1B OR OIAS2
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91232962; PubMed=1709495;
 RA Rutherford M.N., Kumar A., Nissim A., Chebath J., Williams B.R.G.;
 RT "The murine 2-5A synthetase locus: three distinct transcripts from two
 RT linked genes";
 RL Nucleic Acids Res. 19:1917-1924(1991).
 CC -1- FUNCTION: THE 2-5A SYSTEM (THE OAS, 2-5A, AND RNASE L) MAY PLAY A
 CC ROLE IN MEDIATING RESISTANCE TO VIRUS INFECTION, CONTROL OF CELL
 CC GROWTH, DIFFERENTIATION, AND APOPTOSIS.
 CC -1- CATALYTIC ACTIVITY: BINDS DOUBLE-STRANDED RNA AND POLYMERIZES ATP
 CC INTO PPP(A2'P5'A)N OLIGOMERS, WHICH ACTIVATE THE LATENT RNASE L
 CC THAT, WHEN ACTIVATED, CLEAVES SINGLE-STRANDED RNAS.
 CC -1- INDUCTION: BY INTERFERONS.
 CC -1- SIMILARITY: BELONGS TO THE 2-5A SYNTHETASE FAMILY.
 CC
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 CC
 CC EMBL; X55982; CAA39455.1; -
 CC MGI; 97430; Oas1b.
 CC InterPro: IPR001797; 25A_synth.
 CC InterPro: IPR001201; PAP_25A_core.
 CC PROSITE; PS00832; 25A_SYNTH_1; PARTIAL.
 CC PROSITE; PS00833; 25A_SYNTH_2; PARTIAL.
 CC PROSITE; PS0152; 25A_SYNTH_3; 1.
 CC RNA-binding; Transferase; Nucleotidyltransferase;
 CC Interferon induction.
 CC NON_TER 1
 CC NON_TER 192 192
 CC SEQUENCE 192 AA; 21936 MW; 4E1C011EF9024F46 CRC64;

Query Match 9.68; Score 78.5; DB 1; Length 192;
 Best Local Similarity 23.28; Pred. No. 1.8;
 Matches 42; Conservative 25; Mismatches 49; Indels 65; Gaps 9;

QY 3 GKLESKLSVIRN-----LNDQVLFDGNGRPLFEDMTDSDCRDNPRTFIISMVKD 54
 Db 11 GRSDADLVFLNNLTSPEDQLNQGVLIKEIKQLCEVQHERRC----- 54
 QY 55 SQPRGMVNTSVKCEKTSILSCENKIISFKEMNPPDNKOTKSDII----- 100

Db 55 -----GVKFEVHSLRSPNSRALSFK--LSAPDLLKEVKFDVLPAYDLLDLHLNLKK 103
 QY 101 -----FFQOR---SYP-GHDNKMOPFESSYEGYFACE--KERDLFKLI-----LKKEDELG 145
 Db 104 PNQOFYANLISGVPAKREGKLSCTCFMGLQYFLNCRPTKRLRLRLVTHWYQLCKE-KLG 162

QY 146 D 146
 Db 163 D 163

RESULT 11
 IL1A_HORSE STANDARD; PRT; 270 AA.
 AC Q28385; Q77743;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Interleukin-1 alpha precursor (IL-1 alpha).
 GN IL1A.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96131982; PubMed=8578682;
 RA Kato H., Ohashi T., Nakamura N., Nishimura Y., Watari T., Goitsuka R.,
 RA Tsujimoto H., Hasegawa A.;
 RT "Molecular cloning of equine interleukin-1 alpha and -beta cDNAs";
 RL Vet. Immunol. Immunopathol. 48:221-231(1995).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=98285941; PubMed=9622738;
 CC Howard R.D., McIlwraith C.W., Trotter G.W., Nyborg J.K.;
 CC "Cloning of equine interleukin-1 alpha and equine interleukin-1 beta
 CC and determination of their full-length cDNA sequences";
 CC Am. J. Vet. Res. 59:704-711(1998).
 CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
 CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
 CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
 CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS
 CC (BY SIMILARITY).
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
 CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
 CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
 CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
 CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
 CC SECRETORY PROTEINS.
 CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
 CC
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 CC
 CC EMBL; D42146; BAA07717.1; -
 CC EMBL; U92480; AAC39255.1; -
 CC HSP; P01583; IL1A.
 CC InterPro: IPR002348; IL1_HBGF.
 CC InterPro: IPR000975; Interleukin_1.
 CC InterPro: IPR003502; Interleukin_1_prop.
 CC Pfam; PF00340; IL1; 1.
 CC Pfam; PF02394; IL1_propep; 1.
 CC PRINTS; PR00262; IL1HBGF.
 CC SMART; SM00125; IL1; 1.
 CC PROSITE; PS00253; INTERLEUKIN_1; 1.

```
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 112 BY SIMILARITY.
FT CHAIN 113 270 INTERLEUKIN-1 ALPHA.
FT CARBOHYD 141 141 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 110 110 R -> K (IN REF. 2).
FT CONFLICT 150 150 G -> V (IN REF. 2).
SQ SEQUENCE 270 AA; 30806 MW; 381859713754DB90 CRC64;

Query Match
Best Local Similarity 9.5%; Score 77.5; DB 1; Length 270;
Matches 28; Conservative 31; Mismatches 60; Indels 11; Gaps 4;

QY 7 SKLSVIRNLNDQVLFDGQNRPLFEDMTDSCDRNAPRTI-----FILSMYKDSOPRGMA 61
DB 122 TKNYEMRIVNHQCTLNDALNQSIVRDTSGQYLATLALNLDVAFDVGATSEDSQLP 181
QY 62 VTISVKCEKISI-LSCENKIISFKEM-NPPDNIKPTKSDIIFQSVFPHGNKMFESS 119
DB 182 VTLRISKTRLFVSAQNEDEPVLKEMPTPKTIKDTNLLFWER----HGSKNYFKSVA 237
QY 120 YEGYELACEK 129
DB 238 HPKLFIAATKQ 247

RESULT 12
ECM_HUMAN STANDARD; PRT; 1228 AA.
AC Q13201;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Endothelial cell multimerin precursor.
GN MMRN OR ECM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 368-376.
RC TISSUE=Endothelial cells;
RA Hayward C.P.M., Hassell J.A., Denomme G.A., Rachubinski R.A.,
RA Brown C., Kelton J.G.;
RT "The cDNA sequence of human endothelial cell multimerin. A unique
RT protein with RGDS, coiled-coil, and epidermal growth factor-like
RT domains and a carboxyl terminus similar to the globular domain of
RT complement C1q and collagen type VIII and X."
RL J. Biol. Chem. 270:18246-18251(1995).
CC -1- FUNCTION: CARRIER PROTEIN FOR PLATELET (BUT NOT PLASMA) FACTOR
CC V/Va. MAY PLAY A ROLE IN THE STORAGE AND STABILIZATION OF FACTOR V
CC IN PLATELETS.
CC -1- SUBUNIT: MULTIMERIC. COMPOSED OF VARYING SIZED, DISULFIDE-LINKED
CC MULTIMERS, THE SMALLEST OF WHICH IS A HOMOTRIMER. PROTEOLYSIS OF
CC THE PROMULTIMERIN IN THE N-TERMINAL REGION, LEADS TO THE MATURE
CC P155 FORM THAT IS STORED IN PLATELETS.
CC -1- TISSUE SPECIFICITY: SYNTHESIZED BY ENDOTHELIAL CELLS AND
CC MEGAKARYOCYTES. STORED IN PLATELET ALPHA GRANULES AND ENDOTHELIAL
CC CELL WEIBEL-PALADE BODIES, FOLLOWING ACTIVATION OF THESE CELLS, IT
CC IS RELEASED AND ATTACHED TO MEGAKARYOCYTES, PLATELETS, ENDOTHELIUM
CC AND SUBENDOTHELIUM OF BLOOD VESSELS. NOT FOUND IN PLASMA. FOUND IN
CC VASCULAR TISSUES SUCH AS PLACENTA, LUNG, AND LIVER.
CC -1- PTM: THE N-TERMINUS IS BLOCKED.
CC -1- PTM: EXTENSIVELY N-GLYCOSYLATED.
CC -1- DISEASE: DEFICIENCY IN MULTIMERIN DUE TO PROTEOLYTIC DEGRADATION
CC WITHIN THE PLATELET ALPHA GRANULES IS ASSOCIATED WITH AN AUTOSOMAL
CC DOMINANT BLEEDING DISORDER (FACTOR V QUEBEC).
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -----
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EMBL; U27109; AAC52065.1; -.
DR MIN; 601456; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001073; C1q.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR Pfam; PF00008; EGF; 1.
DR PRINTS; PR00007; COMPLEWNTC1Q.
DR SMART; SM00110; C1Q; 1.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS01113; C1Q; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
KW Signal; Glycoprotein; EGF-like domain; Coiled coil.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 1228 ENDOTHELIAL CELL MULTIMERIN.
FT DOMAIN 1041 1077 EGF-LIKE.
FT DOMAIN 1119 1149 C1Q.
FT DOMAIN 333 365 COILED COIL (POTENTIAL).
FT DOMAIN 400 430 COILED COIL (POTENTIAL).
FT DOMAIN 503 523 COILED COIL (POTENTIAL).
FT DOMAIN 580 650 COILED COIL (POTENTIAL).
FT DOMAIN 675 726 COILED COIL (POTENTIAL).
FT DOMAIN 819 869 COILED COIL (POTENTIAL).
FT DOMAIN 309 313 POLY-SR.
FT SITE 186 188 CELL ATTACHMENT SITE (POTENTIAL).
FT DISULFID 1045 1056 BY SIMILARITY.
FT DISULFID 1050 1065 BY SIMILARITY.
FT CARBOHYD 21 21 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 120 120 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 344 344 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 431 431 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 507 507 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 541 541 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 576 576 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 618 618 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 680 680 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 729 729 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 783 783 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 828 828 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 840 840 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 921 921 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 933 933 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 942 942 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 981 981 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1020 1020 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1075 1075 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 1228 AA; 138071 MW; EAA98B0A17E2C4CD CRC64;

Query Match
Best Local Similarity 9.5%; Score 77.5; DB 1; Length 1228;
Matches 32; Conservative 37; Mismatches 46; Indels 35; Gaps 9;

QY 1 YFGKLESKLSVIRNLNDQVL-----FDGQNRPLFEDMTD-----SDCRDNAPR-TIFII 49
DB 502 YVESLTKTLKSLKEVHEQLLSTEQVSDQKNAPAAESVNNVTEYWTSLHENIKKQSLMWL 561
QY 50 SMYKD---SQPRGMVAVTSVCKEKISII-SCENKI-----ISFKEMNPPDN---IKDTK 96
DB 562 QMFEDLHQESKINNLTVSLMEKESLRGECEDMLSKCRNDFQKFKQDKTEENLHVLNQTLL 621
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QY 97 SDIIFORSVPGHDKM-----QFESSYE 121
DB 622 AEVLFF-----PMDNKMCKMSEQLNDLTYD 645

RESULT 13
RAG2_HUMAN STANDARD; PRT; 527 AA.
ID RAG2_HUMAN STANDARD; PRT; 527 AA.
AC P55895;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE V(D)J recombination activating protein 2 (RAG-2).
GN RAG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=93052553; PubMed=1428003;
RA Ichihara Y., Hirai M., Kurosawa Y.;
RT "Sequence and chromosome assignment to 11p13-p12 of human RAG genes.";
RL Immunol. Lett. 33:277-284(1992).
RN [2]
RP SEQUENCE OF 318-411 FROM N.A.
RX MEDLINE=92003959; PubMed=1832998;
RA Borjes J.C., Cayuela J.M., Loiseau P., Sigaux F.;
RT "Expression of human recombination activating genes (RAG1 and RAG2)
RT in neoplastic lymphoid cells: correlation with cell differentiation
RT and antigen receptor expression.";
RL Blood 78:2053-2061(1991).
RN [3]
RP VARIANTS SCID GLN-229 AND TYR-478.
RX MEDLINE=96412253; PubMed=8810255;
RA Schwarz K., Gauss G.H., Ludwig L., Pannicke U., Li Z., Linder D.,
RA Friedrich W., Seger R.A., Hansen-Hagge T.E., Desiderio S.,
RA Lieber M.R., Bartram C.R.;
RT "RAG mutations in human B cell-negative SCID.";
RL Science 274:97-99(1996).
RN [4]
RP VARIANTS OS TRP-41 AND ARG-285.
RX MEDLINE=98292185; PubMed=9630231;
RA Villa A., Santagata S., Bozzi F., Gilliani S., Frattini A., Imberti L.,
RA Gatta L.B., Ochs H.D., Schwarz K., Notarangelo L.D., Vezzoni P.,
RA Spanopoulou E.;
RT "Partial V(D)J recombination activity leads to Omenn syndrome.";
RL Cell 93:885-896(1998).
CC -1- FUNCTION: DURING LYMPHOCYTE DEVELOPMENT, THE GENES ENCODING
CC IMMUNOGLOBULINS AND T CELL RECEPTORS ARE ASSEMBLED FROM VARIABLE
CC (V), DIVERSITY (D), AND JOINING (J) GENE SEGMENTS. THIS
CC COMBINATORIAL PROCESS, KNOWN AS V(D)J RECOMBINATION, ALLOWS THE
CC GENERATION OF AN ENORMOUS RANGE OF BINDING SPECIFICITIES FROM A
CC LIMITED AMOUNT OF GENETIC INFORMATION. THE RAG1/RAG2 COMPLEX
CC INITIATES THIS PROCESS BY BINDING TO THE CONSERVED RECOMBINATION
CC SIGNAL SEQUENCES (RSS) AND INTRODUCING A DOUBLE-STRAND BREAK
CC BETWEEN THE RSS AND THE ADJACENT CODING SEGMENT. THESE BREAKS ARE
CC GENERATED IN TWO STEPS, NICKING OF ONE STRAND (HYDROLYSIS),
CC FOLLOWED BY HAIRPIN FORMATION (TRANSESTERIFICATION). RAG1/2 HAS
CC ALSO BEEN SHOWN TO FUNCTION AS A TRANSPOSASE IN VITRO, AND TO
CC POSSESS RSS-INDEPENDENT ENDONUCLEASE ACTIVITY (END PROCESSING) AND
CC HAIRPIN OPENING. RAG1 ALONE CAN BIND TO RSS BUT STABLE, EFFICIENT
CC BINDING REQUIRES RAG2. ALL KNOWN CATALYTIC ACTIVITIES REQUIRE THE
CC PRESENCE OF BOTH PROTEINS.
CC -1- SUBUNIT: THE RAG COMPLEXES APPEAR TO CONTAIN THREE TO FIVE
CC MOLECULES OF RAG2 FOR EACH MOLECULE OF RAG1.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: CELLS OF THE B AND T LYMPHOCYTE LINEAGES.
CC -1- DISEASE: DEFECTS IN RAG2 ARE A CAUSE OF SEVERE COMBINED
CC IMMUNODEFICIENCY, B CELL-NEGATIVE (B(-) SCID).
CC -1- DISEASE: DEFECTS IN RAG2 ARE A CAUSE OF OMENN SYNDROME (OS); A

SEVERE IMMUNODEFICIENCY CHARACTERIZED BY THE PRESENCE OF
ACTIVATED, ANERGIC, OLIGOCLONAL T CELLS, HYPEROSINOPHILIA, AND
HIGH IGE LEVELS.
-1- DATABASE: NAME=RAG2base; NOTE=RAG2 deficiency database;
WWW="http://www.uta.fi/inf/bioinfo/RAG2base/"
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CC EMBL; M94633; -; NOT_ANNOTATED_CDS.
CC MIM; 179616; -;
CC MIM; 601457; -;
CC MIM; 603554; -;
CC InterPro; IPR004321; RAG2.
CC Pfam; PF03089; RAG2; 1.
CC Hydrolase; Endonuclease; Nuclear protein; DNA-binding;
KW DNA recombination; Disease mutation.
FT VARIANT 41 41 C->W (IN OS).
FT VARIANT 229 229 R->Q (IN B(-) SCID).
FT VARIANT 285 285 M->R (IN OS).
FT VARIANT 478 478 C->Y (IN B(-) SCID).
FT SEQUENCE 527 AA; 59241 MW; ICC4D0F8635BA87 CRC64;
SQ
Query Match 9.4%; Score 76.5; DB 1; Length 527;
Best Local Similarity 28.9%; Pred. No. 9.3;
Matches 26; Conservative 10; Mismatches 31; Indels 23; Gaps 4;
QY 72 SILSCENKIKSFKEPNPPONIKTKSDIIFQRS-----VPGHDKMKQFESSYEG 122
DB 288 NIISLEDNKIEIREMETPTDTPDIKHSKIWFSGSNMGNTVFLGIPG-DNK-QVVSEGFYF 345
QY 123 YFLACEKERDLFLKILKKEDELGDRSIMFT 152
DB 346 YMLKC-----AEDDTNEEQTTFT 363
RESULT 14
Y414_MYCGE STANDARD; PRT; 1036 AA.
AC P47653; P47654; Q49457;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG414.
GN MG414.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchmann J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA Nguyen D.T., Uterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Bost K.F., Hu P.-C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium.";
RL Science 270:397-403(1995).
RN [2]
RP SEQUENCE OF 52-146 AND 733-833 FROM N.A.

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```
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=94075230; PubMed=8253680;
RA Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
RT "A survey of the Mycoplasma genitalium genome by using random
RL sequencing.";
RL J. Bacteriol. 175:7918-7930(1993).
CC -|- SIMILARITY: BELONGS TO THE MG414 / MG415 FAMILY.
CC -----
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CC -----
DR EMBL; U39723; AAC71641.1; -.
DR EMBL; U01695; AAB01008.1; -.
DR EMBL; U01804; AAD12330.1; -.
DR TIGR; MG414; -.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 4 24
FT TRANSMEM 1004 1024
FT CONFLICT 733 736
FT CONFLICT LEPT -> SRAS (IN REF. 2).
SQ SEQUENCE 1036 AA; 123179 MW; 12A21F00F686A141 CRC64;

Query Match          9.4%; Score 76.5; DB 1; Length 1036;
Best Local Similarity 21.9%; Pred. No. 21;
Matches 33; Conservative 33; Mismatches 64; Indels 21; Gaps 6;

QY 14 NLNDQVLFIDQGNRPLFED--MTSDSCRDNAPRTIFIISMYKDSQPRGMVATISVKCEKI 71
DB 845 SLNDEQLLVKLNITLSEKRLQTTNVRFNLNKKNKFNTHLVNKNQFNLFVDVRSKRL 904
QY 72 SI--LSCENKIISFKEMPPDNKDKSDIIFQFORSVPGHDKMKQFESSSEYGYFLACEK 129
DB 905 FIKGVNNDNQVSIY-----DLKITNNQTLIV-DANGFDNSIWFDTIS-----EN 950
QY 130 ERDLFKLI---LKKEDELGDRSIMFTVQNEED 157
DB 951 QTQLFKAUSFYLKQNNLOPKRVDPFNLSQD 981

RESULT 15
CENE_HUMAN
ID CENE_HUMAN STANDARD; PRT; 2663 AA.
AC Q02224;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Centromeric protein E (CENP-E protein).
GN CENPE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93024922; PubMed=1406971;
RA Yen T.J., Li G., Schaar B.T., Szilak I., Cleveland D.W.;
RT "CENP-E is a putative kinetochore motor that accumulates just before
RT mitosis.";
RL Nature 359:536-539(1992).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=95196755; PubMed=7889940;
RA Thrower D.A., Jordan M.A., Schaar B.T., Yen T.J., Wilson L.;
RT "Mitotic HeLa cells contain a CENP-E-associated minus end-directed
RT microtubule motor.";
RL EMBO J. 14:918-926(1995).
RN [3]
RP CHARACTERIZATION.
```

```
RX MEDLINE=98437347; PubMed=9763420;
RA Chan G.K.T., Schaar B.T., Yen T.J.;
RT "Characterization of the kinetochore binding domain of CENP-E reveals
RT interactions with the kinetochore proteins CENP-F and HUBB1.";
RL J. Cell Biol. 143:49-63(1998).
CC -|- FUNCTION: MINUS-END DIRECTED MICROTUBULE MOTOR. PROBABLE
CC KINETOCHORE MOTOR. ACCUMULATES JUST BEFORE MITOSIS AT THE G2 PHASE
CC OF THE CELL CYCLE. PROBABLY IMPORTANT FOR CHROMOSOME MOVEMENT
CC AND/OR SPINDLE ELONGATION.
CC -|- SUBUNIT: INTERACTS WITH CENP-F AND BUBR1 KINASE.
CC -|- SUBCELLULAR LOCATION: ASSOCIATES WITH KINETOCHORES DURING
CC CONGRESSION, RELOCATES TO THE SPINDLE MIDZONE AT ANAPHASE, AND IS
CC QUANTITATIVELY DISCARDED AT THE END OF THE CELL DIVISION.
CC -|- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL; Z15005; CAA78727.1; -.
DR PIR; S28261; S28261.
DR HSSP; P17119; 3KAR.
DR MIM; 117143; -.
DR InterPro; IPR001752; kinesin.
DR Pfam; PF00225; kinesin_1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC.1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
KW Motor protein; Cell division; ATP-binding; Coiled coil; Mitosis;
KW Cell cycle; Centromere.
FT DOMAIN 1 335
FT DOMAIN 336 2471
FT DOMAIN 2472 2663
FT NP_BIND 86 93
FT ATP (BY SIMILARITY).
SQ SEQUENCE 2663 AA; 312087 MW; CFC13880C8C8CB8 CRC64;

Query Match          9.2%; Score 75; DB 1; Length 2663;
Best Local Similarity 20.6%; Pred. No. 90;
Matches 37; Conservative 38; Mismatches 69; Indels 36; Gaps 7;

QY 4 KLESKLSVIRNLNDQVLFIDQGNRPL--FEDMTSDSCRDNAPRTIFIISMYKDSQPRGMA 61
DB 916 KLQQTLEEVKTLTQEKDDLKQLQESLQTERDQLKSDIHD-----VNMNIDTQQLRN 968
QY 62 VTISVKCEKISILSCENKIIS--FKEMPPDNKDKSDIIFQFORSVPGHDKMKQFESS 119
DB 969 ALESLSKHQETINTLTKSISEVSRNLHMEENTGETKDE---FOQKMGVIGDKKODLEAKN 1025
QY 120 YGYEPL-----ACEKRDLFKLILKK-----EDELGDR-----SIMFTVQNEED 157
DB 1026 TOTLTADVKNDEITEEQRKIFSLIOEKNELOQMLESVAEKEQLKTDLENIENTIENQE 1085

Search completed: October 8, 2002, 10:17:03
Job time: 189 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 8, 2002, 10:13:29 ; Search time 43.19 Seconds
(without alignments)
628.854 Million cell updates/sec

Title: SEQ6ILEAT73
Perfect score: 815
Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKDELGDRSIMFTVQNE 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phase:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_virus:
16: sp_bacteriap:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	797	97.8	193	4 Q96KJ8	Q96KJ8 homo sapien
2	791	97.1	193	6 Q9BG15	Q9BG15 macaca mula
3	653	80.1	178	6 Q9M2L8	Q9M2L8 bos taurus
4	647	79.4	193	6 Q9GL09	Q9GL09 ovis aries
5	633	77.7	192	6 Q95M33	Q95M33 felis silve
6	625	76.7	192	6 Q9N1P7	Q9N1P7 sus scrofa
7	440	54.0	196	11 Q91Z66	Q91Z66 sigmodon hi
8	312	38.3	84	6 Q95LE7	Q95LE7 canis famil
9	204	25.0	45	4 Q9NO49	Q9NO49 homo sapien
10	193	23.7	211	13 Q98S01	Q98S01 anas platyr
11	182.5	22.4	198	13 Q918D2	Q918D2 gallus gall
12	91	11.2	4643	5 Q9VW71	Q9VW71 drosophila
13	84	10.3	381	3 O43031	O43031 schizosacch
14	84	10.3	452	16 O25249	O25249 helicobacte
15	83.5	10.2	866	16 O84500	O84500 chlamydia t
16	82.5	10.1	1049	2 Q93KF0	Q93KF0 caldcellul

17	82	10.1	263	3	O74316	schizosacch
18	82	10.1	364	16	O9PM33	campylobact
19	81.5	10.0	617	5	O25986	plasmodium
20	81	9.9	1044	5	O94173	pneumocysti
21	80.5	9.9	454	6	O9BGD1	micronycter
22	80	9.8	847	4	O9NUC1	homo sapien
23	79.5	9.8	454	6	O9BGA4	erophylla s
24	79.5	9.8	454	6	O9BGA8	sturnira li
25	79	9.7	632	10	O80569	arabidopsis
26	78.5	9.6	454	6	O9BGB7	phyllostomu
27	78	9.6	445	13	O57610	scylliorhinu
28	78	9.6	473	5	O16673	caenorhabdi
29	77.5	9.5	454	6	O9BGB8	phyllonycte
30	76.5	9.4	137	5	O77077	plasmodium
31	76.5	9.4	204	2	O9ZNJ7	ciostidium
32	76.5	9.4	454	6	O9BGE3	furipeterus
33	76.5	9.4	454	6	O9BGD7	lonchorhina
34	76.5	9.4	454	6	O9BGD5	macrotus ca
35	76.5	9.4	595	10	O9SDM4	dunaliella
36	76	9.3	273	10	O9LM98	arabidopsis
37	76	9.3	450	16	O9ZLW8	helicobacte
38	76	9.3	614	10	O9LAW0	arabidopsis
39	76	9.3	747	10	O82393	arabidopsis
40	75.5	9.3	454	6	O9BDE1	micronycter
41	75.5	9.3	454	6	O9BGF9	ariteus fla
42	75.5	9.3	454	6	O9BGE7	diphylla ec
43	75.5	9.3	454	6	O9BGD6	macrophyllu
44	75.5	9.3	454	6	O9BGD4	macrotus wa
45	75.5	9.3	454	6	O9BGD3	macrotus wa

ALIGNMENTS

RESULT 1

Q96KJ8 PRELIMINARY; PRT; 193 AA.
AC O96KJ8;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE INTERLEUKIN 18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ying P., Jianxin L.;
RT "Cloning of Mutant Human Interleukin 18 cDNA."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF380360; AAK57024.1; -
SQ SEQUENCE 193 AA; 22323 MW; 2E500205D1B7E5F7 CRC64;

Query Match 97.8%; Score 797; DB 4; Length 193;
Best Local Similarity 97.5%; Pred. No. 1.7e-72;
Matches 153; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy	1	YFGKLESKLSVIRNLNDQVLFDQGNRPLFEDMTDSCDRDNAPRTFIISMYKDSQPRGM	60
Db	37	YFGKLESKLSVIRNLNDQVLFDQGNRPLFEDMTDSCDRDNAPRTFIISMYKDSQPRGM	96
Qy	61	AVTISVKCEKISILSCENKIISFKEMNPPDNIKDKTSIIFFQRSVPVPGHDKMKQFESSY	120
Db	97	AVTISVKCEKISTLSCENKIISFKVNPPDNIKDKTSIIFFQRSVPVPGHDKMKQFESSY	156
Qy	121	EGYFTACKEKRDFLKILKKEDELGDRSIMFTVQNE 157	
Db	157	EGYFTCEKERDFLKILKKEDELGDRSIMFTVQNE 193	
RESULT	2		


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RA Hanlon L., McGillivray C.P., Argyle D.J.A., Nicolson L., Onions D.E.;
RT "Nucleotide sequence of feline IGf cDNA (provisional).";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y13923; CAC42918.1; -.
SQ SEQUENCE 192 AA; 22068 MW; 5878C3DAC7A43358 CRC64;

Query Match 77.7%; Score 633; DB 6; Length 192;
Best Local Similarity 76.4%; Pred. No. 5.4e-56;
Matches 120; Conservative 21; Mismatches 16; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRNAPRTFIISMYKDSQPRGM 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 36 YFGKLEHKLILRNLDQVLFIDQGNRPFLFEDMTSDCDRNAPRTFIISMYKDSLTRGL 95
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 AVTISVKCEKISILSCENKIIIFKEMNPPDNIDKTKSDIIFQRSVPGHDKMQFESSY 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 96 AVTISVNYKMTSLCKNQIIIFKEMSPPEINDEGNDIIFQRSVPGHDDKIQFESSLY 155
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 156 KGYFLACEKERDLFKLILKKEDELGDRSIMFTVQKN 192
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 6
Q9NIP7 PRELIMINARY; PRT; 192 AA.
AC Q9NIP7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE INTERLEUKIN-18.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG.
RX MEDLINE=20356335; PubMed=10901174;
RA Oem J.K., Song H.J., Kang S.W., Jeong W.S.;
RT "Cloning, sequencing, and expression of porcine interleukin-18 in
RT Escherichia coli.";
RL Mol. Cells 10:343-347(2000).
DR EMBL: AF176949; AAF35169.1; -.
DR InterPro: IPR000975; Interleukin_1.
DR SMART: SM00125; IL1; 1.
SQ SEQUENCE 192 AA; 21969 MW; A51EB7A4E221A16D CRC64;

Query Match 76.7%; Score 625; DB 6; Length 192;
Best Local Similarity 73.9%; Pred. No. 3.4e-55;
Matches 116; Conservative 25; Mismatches 16; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRNAPRTFIISMYKDSQPRGM 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 36 YFGKLEPKLSIIRNLNDQVLFIDQGNRPFLFEDMTSDCDRNAPRTFIISMYKDSLTRGL 95
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 AVTISVKCEKISILSCENKIIIFKEMNPPDNIDKTKSDIIFQRSVPGHDKMQFESSY 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 96 AVTISVQCKMTSLCKNTLSFKEMSPPDIDDEGNDIIFQRSVPGHDDKIQFESSLY 155
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 156 KGYFLACKRENDFLKILKKEDECGDKSITFTVQSKN 192
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
Q91266 PRELIMINARY; PRT; 196 AA.
AC Q91266;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
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DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE INTERLEUKIN 18.
GN IL18.
OS Sigmodon hispidus (hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmodon.
OX NCBI_TaxID=42415;
RN [1]
RP SEQUENCE FROM N.A.
RA Blanco J.C., Pletneva L.M., Prince G.A.;
RT "Sigmodon hispidus cytokines, chemokines and interferons.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY059406; AAL26703.1; -.
SQ SEQUENCE 196 AA; 22545 MW; E27C5BDC397F951C CRC64;

Query Match 54.0%; Score 440; DB 11; Length 196;
Best Local Similarity 59.4%; Pred. No. 1.5e-36;
Matches 92; Conservative 24; Mismatches 37; Indels 2; Gaps 2

QY 2 FGLKESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRNAPRTFIISMYKDSQPRGM 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 39 FFKESSTTAVIRNMNDYVLFIDREKSPVFEDMPDADQKANEACTRLIYIYMTDFNPGGL 98
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 AVTISVKCEKISILSCENKIIIFKEMNPPDNIDKTKSDIIFQRSVPGHDKMQFESSY 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 99 PVTLSVRDRTMTSLCKNQIIIFKEMPPLEIDGTGKSDLIIFQRAVPGH-NKKMFESSLH 157
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQN 155
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 158 EGHFLACERDGSFKLILKKEDELGDRSIMFTVQN 192
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
Q95LE7 PRELIMINARY; PRT; 84 AA.
AC Q95LE7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE IL-18 (FRAGMENT).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD.
RA Chamizo C., Rubio J.M., Moreno J., Alvar J.;
RT "Semi-quantification of canine cytokine expression by one tube RT-
RT PCR.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF327900; AAL26920.1; -.
FT NON_TER 1 84
FT NON_TER 84 84
SQ SEQUENCE 84 AA; 9568 MW; 19BD9E27F336774B CRC64;

Query Match 38.3%; Score 312; DB 6; Length 84;
Best Local Similarity 74.7%; Pred. No. 4.2e-24;
Matches 59; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRNAPRTFIISMYKDSQPRGM 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 5 YFGKLEPKLSIIRNLNDQVLFIDQGNRPFLFEDMPDSDCTDNAPHTFIYIYMYKDSLTRGL 64
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 AVTISVKCEKISILSCENK 79
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 65 AVTISVKYKMTSLCKNK 83
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
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Q9NQ49
ID Q9NQ49 PRELIMINARY; PRT; 45 AA.
AC Q9NQ49;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE INTERLEUKIN-18 (FRAGMENT).
GN IL-18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Farhan A.J., Pravica V., Hutchinson I.V.;
RT "Identification of Human Interleukin-18 gene polymorphisms.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ295724; CAC01436.1; -
FT NON_TER 1 45
FT TER 45 45
SQ SEQUENCE 45 AA; 5266 MW; DF3A626507E3D61A CRC64;

Query Match 25.08; Score 204; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDVLFIDOGNRPFLFEDMTDSDCR 39
Db 7 YFGKLESKLSVIRNLNDVLFIDOGNRPFLFEDMTDSDCR 45

RESULT 10
Q98SQ1
ID Q98SQ1 PRELIMINARY; PRT; 211 AA.
AC Q98SQ1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE INTERLEUKIN-18 (FRAGMENT).
GN IL-18.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RA Chan W.-S., Warr G.W., Middleton D.L., Lundquist M.L., Higgins D.A.;
RT "Anas platyrhynchos T-cell antigens, IL-18 gene.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF336122; AAK26322.1; -
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
FT NON_TER 1 1
FT TER 1 1
SQ SEQUENCE 211 AA; 24541 MW; CA6FC63538211B2B CRC64;

Query Match 23.7%; Score 193; DB 13; Length 211;
Best Local Similarity 36.5%; Pred. No. 1.2e-11;
Matches 61; Conservative 29; Mismatches 63; Indels 14; Gaps 9;

QY 2 FGKLESKLSVIRNLNDVLFIDOG- NRPLFEDMTDSDCRNAPRTIFISMYKDSQP-RG 59
Db 43 FSREKTLHLRLNNSQVLRPLDNLAAAFEDVTQDEKSGSGMN-FCMCYKTTTTSAG 101

QY 60 MAVTISVKCE-KISILSCENK-----IISFKEMNPDPNDIKTSDIIFQSRVPGHDK-M 113
Db 102 MPVAFSRVEDKSYMCCEEEHGKMWVRFEQVPEKIPG-ESNIIFFKKTFTSYSSKAF 160

QY 114 QFESSSYEGYFLACEKEDFLKILKK---EDELGDRS-IMFTVQNE 156
Db 161 KFEYSLEGRMFLAFEEEDSLRKLILKLPLREDEVDETTKTTLTSHNE 207
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RESULT 11
Q918D2
ID Q918D2 PRELIMINARY; PRT; 198 AA.
AC Q918D2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INTERLEUKIN 18.
GN IL-18.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20508574; PubMed=11054275;
RA Schneider K., Puehler F., Baeuerle D., Elvers S., Staeheli P.,
RA Kaspers B., Weining K.C.;
RT "cDNA cloning of biologically active chicken Interleukin-18.";
RL J. Interferon Cytokine Res. 20:879-883(2000).
DR EMBL; AJ277865; CAB96214.1; -
FT CHAIN 30 198 INTERLEUKIN 18.
FT TER 198
SQ SEQUENCE 198 AA; 22918 MW; 29BB77DC3E3C6600 CRC64;

Query Match 22.4%; Score 182.5; DB 13; Length 198;
Best Local Similarity 36.8%; Pred. No. 1.2e-10;
Matches 57; Conservative 25; Mismatches 60; Indels 13; Gaps 7;

QY 13 RNLDQVLFIDOG- NRPLFEDMTDSDCRNAPRTIFISMYKDSQP-RGMATVISVKCEK 70
Db 42 RVNSQLLVPRDLNVAFAEDVTQDEVKSGS-GMYFDIHCYKTTAPSGMPVATSVQVED 100

QY 71 ISILSCENK-----IISFKEMNPDPNDIKTSDIIFQSRVPGHDK-MQFESSSYEGYF 124
Db 101 KSYVMCCKEHGMVVRFEQVPEKIPG-ESNIIFFKKTFTSCSSKAFKPEYSLEQGMF 159

QY 125 LACEKERDLFLKILKK---EDELGDRS-IMFTVQNE 156
Db 160 LAFEEEDSLRKLILKLPLREDEVDETTKTTLTSHNE 194

RESULT 12
Q9VW71
ID Q9VW71 PRELIMINARY; PRT; 4643 AA.
AC Q9VW71;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE PUTATIVE FAT-LIKE CADHERIN PRECURSOR (CG7749 PROTEIN).
GN CG7749.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BERKELEY;
RA MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
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RESULT 13
O43031 PRELIMINARY; PRT; 381 AA.
AC O43031; Q9US93;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 44.2 KDA PROTEIN C3B9.02C IN CHROMOSOME II.
GN SPBC3B9.02C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Wood V., Rajandream M.A., Barrell B.G., Skelton J., Churcher C.M.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 140-321 FROM N.A.
RC STRAIN=968 H90;
RA Ding D.;
RT "Generation and analysis of GFP-gene fusion library of fission
   yeast.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO C.ELEGANS R11A8.2.
DR EMBL; AL022070; CAA17782.1; -.
DR EMBL; AB027944; BAA87248.1; -.
DR InterPro; IPR000467; G_patch.
DR SMART; SM00443; G_patch; 1.
KW Hypothetical protein
SQ SEQUENCE 381 AA; 44214 MW; E1542538B667549F CRC64;

Query Match 10.3%; Score 84; DB 3; Length 381;
Best Local Similarity 26.4%; Pred. No. 2.2;
Matches 39; Conservative 23; Mismatches 54; Indels 32; Gaps 7;

QY 3 GKLESKLSVTRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPGMAV 62
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 208 GOLSSKDAF--DVNQRPTEFLGMAKPVDSLTETDIWKPKTKMF----- 250
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 63 TISVK-CEKISILSCENKIISF-KEMNPPDNKDTSDIIFFORSVPGHDKMQFESSY 120
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 251 -LPVKPLESALNSQNEHTVEOKKSIDNL--TPSELFRKRS---RDNNLSRSS-- 302
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 EGYFLACEKERDLFKILKKEDELGDRS 148
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 303 -----VSSKHLDYNSRNYNKRDRDPDPT 325
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
O25249 PRELIMINARY; PRT; 452 AA.
AC O25249;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 52.7 KDA PROTEIN.
GN HP0508.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=922185;
RA Tomb J.-F., White O., Keriavage A.R., Clayton R.A., Sutton G.G.,
   Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
   Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,

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RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
   pylori.";
RL Nature 388:539-547(1997).
DR EMBL; AF000565; AAD07578.1; -.
DR TIGR; HF0508; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 452 AA; 52655 MW; E2F88D85EC9EDB92 CRC64;

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Query Match 10.3%; Score 84; DB 16; Length 452;
Best Local Similarity 24.4%; Pred. No. 2.6;
Matches 41; Conservative 30; Mismatches 71; Indels 26; Gaps 8;

QY 9 LSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPR----- 58
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 105 LVYFRQFNNOA-FLIAPNDELYEQIRATNTDINFISDDLVTFLNGPDPKIANLRKACNV 163
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 59 -GMAYTISVKCEKISILSCEN-KIISFKEMNPPDNKDTSDIIFFORSVPGHD-----NK 112
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 164 YSVGVIIVTNTNLILSCSFELKREL---DTSGVTKTSTPFSR-VEGIDAGTLGK 219
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 113 MQFESSYEGYF-----LACEKERDLFKILKKEDELGDRSIMFTVQNE 156
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 220 L-FSGSQSKNYFAYDALYVKKEKRVIRKKREKIDSRKREIKREIKOE 266
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 15
O84500 PRELIMINARY; PRT; 866 AA.
AC O84500;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DNA POLYMERASE I.
GN POLA OR CT493.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UW-3/CG;
RX MEDLINE=99000809; PubMed=9784136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
   Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
   Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
   Chlamydia trachomatis.";
RL Science 282:754-759(1998).
DR EMBL; AF001322; AAC68093.1; -.
DR HSSP; P00582; 1KFS.
DR InterPro; IPR002562; 3_5_exonuclease.
DR InterPro; IPR002421; 5_3_exonuclease.
DR InterPro; IPR002298; DNA_poli.
DR InterPro; IPR001098; DNA_poli.
DR InterPro; IPR000513; Exo_N_I.
DR InterPro; IPR003584; HH2.
DR Pfam; PF01367; 5_3_exonuclease; 1.
DR Pfam; PF02739; 5_3_exonuc_N; 1.
DR Pfam; PF00476; DNA_poli_A; 1.
DR PRINTS; PR00868; DNAPOLI.
DR SMART; SM00474; 35EXOC; 1.
DR SMART; SM00475; 53EXOC; 1.
DR SMART; SM00279; HbH2; 1.
DR SMART; SM00482; POLAC; 1.
KW Complete proteome.
SQ SEQUENCE 866 AA; 96583 MW; A12883E20C309D2D CRC64;

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Query Match      10.2%; Score 83.5; DB 16; Length 866;
Best Local Similarity 26.4%; Pred. No. 6.3;
Matches 34; Conservative 23; Mismatches 27; Indels 45; Gaps 8;

QY 1 YFGKLESKLSVIRNLNDQVLEFI---DOGNRPLFEDMTD-----SDCRDNAPRTIFII 49
Db 441 YFGMLASKLLAIKN---YLFVKLEEKGLKIDIFETVEQPLEAVLFAMEC-----V 486

QY 50 SNYKDSQPRGMV---TISVKCEKIS-----ILSCENKIIISFKEMN-----PPDN 91
Db 487 GMPILDSQ--GLAVLDRDLTKLEECESQEIYDLVGCEFNKSPKQLSDILYQRLGIEPVDK 544

QY 92 IKDTKSDII 100
Db 545 AKSTRAEVL 553

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Search completed: October 8, 2002, 10:16:41
Job time: 192 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 8, 2002, 10:05:29 ; Search time 20.63 seconds
(without alignments)
185.886 Million cell updates/sec

Title: SEQ6ILEAT73

Perfect score: 815

Sequence: 1 YFGKESKLSVIRNLNDQVL.....LKKEDELGDSIRMTFVNQED 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_AA.*
- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	810	99.4	157	2	US-08-896-605A-6
2	810	99.4	157	2	US-08-896-501A-4
3	810	99.4	157	3	US-08-884-324-1
4	810	99.4	157	3	US-08-996-338-26
5	810	99.4	157	4	US-08-558-818-1
6	810	99.4	157	4	US-08-974-469A-1
7	810	99.4	157	4	US-08-832-180-1
8	810	99.4	157	4	US-08-832-198-6
9	810	99.4	193	2	US-08-896-605A-2
10	810	99.4	193	2	US-08-896-501A-2
11	810	99.4	193	4	US-08-832-180-9
12	512	62.8	157	2	US-08-502-535B-2
13	512	62.8	157	2	US-08-908-005A-2
14	512	62.8	157	3	US-08-996-338-27
15	512	62.8	157	4	US-08-558-818-7
16	512	62.8	157	4	US-08-974-469A-7
17	512	62.8	157	4	US-08-832-180-8
18	512	62.8	157	4	US-08-832-198-11
19	512	62.8	157	4	US-09-253-523-2
20	512	62.8	157	4	US-09-251-911-2
21	259	31.8	50	4	US-08-832-198-2
22	96	11.8	25	4	US-08-558-818-4
23	96	11.8	25	4	US-08-974-469A-4
24	96	11.8	25	4	US-08-832-180-4
25	96	11.8	25	4	US-08-832-198-8
26	90	11.0	17	4	US-08-832-198-5
27	83	10.2	155	6	5494663-8

Query Match 99.4%; Score 810; DB 2; Length 157;
Best Local Similarity 99.4%; Pred. No. 7.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ALIGNMENTS

RESULT 1

US-08-896-605A-6

; Sequence 6, Application US/08896605A

; Patent No. 5879942

; GENERAL INFORMATION:

; APPLICANT: TANIMOTO, Tadao

; APPLICANT: KURIMOTO, Masashi

; TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM: disk

; MEDIUM TYPE: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/896,605A

; FILING DATE: 18 July 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 207,691/1996

; FILING DATE: 19-JUL-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 156,062/1997

; FILING DATE: 30-MAY-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: BROWDY, Roger L.

; REGISTRATION NUMBER: 25,618

; REFERENCE/DOCKET NUMBER: TANIMOTO-2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 157 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-896-605A-6

Patent No. 5494663
Sequence 1, Appli
Sequence 13, Appli
Sequence 20, Appli
Sequence 18, Appli
Sequence 14, Appli
Sequence 5, Appli
Sequence 184, App
Sequence 4, Appli
Sequence 11, Appli
Sequence 16, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTTIFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISLSCENKIISFKENPPDNINKDTSKDIFFORSVPGHDNKKMFESSY 120
Db 61 AVTISVKCEKISLSCENKIISFKENPPDNINKDTSKDIFFORSVPGHDNKKMFESSY 120

QY 121 EGYFLACERDLFKLILKKEDELGDRSINFTVQNE 157
Db 121 EGYFLACERDLFKLILKKEDELGDRSINFTVQNE 157

RESULT 2
US-08-896-501A-4
; Sequence 4, Application US/08896501A
; Patent No. 5891663
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 18-JUL-1997
; APPLICATION NUMBER: US/08/896,501A
; PRIORITY APPLICATION DATA:
; FILING DATE: 25-JUL-1996
; APPLICATION NUMBER: JP 213,267/1996
; PRIORITY APPLICATION DATA:
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: JP 31,474/1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO=3
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-896-501A-4

Query Match 99.4%; Score 810; DB 2; Length 157;
Best Local Similarity 99.4%; Pred. No. 7.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTTIFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISLSCENKIISFKENPPDNINKDTSKDIFFORSVPGHDNKKMFESSY 120
Db 61 AVTISVKCEKISLSCENKIISFKENPPDNINKDTSKDIFFORSVPGHDNKKMFESSY 120

QY 121 EGYFLACERDLFKLILKKEDELGDRSINFTVQNE 157
Db 121 EGYFLACERDLFKLILKKEDELGDRSINFTVQNE 157

RESULT 3
US-08-884-324-1
; Sequence 1, Application US/08884324
; Patent No. 6060283
; GENERAL INFORMATION:
; APPLICANT: Takanoori OKURA
; APPLICANT: Kakuji TORIGOE
; APPLICANT: Masahi KURIMOTO
; TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
; OF INDUCING THE PRODUCTION OF INTERFERON-
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 27-JUN-1996
; APPLICATION NUMBER: US/08/884,324
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 185,305/96
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: OKURA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-884-324-1

Query Match 99.4%; Score 810; DB 3; Length 157;
Best Local Similarity 99.4%; Pred. No. 7.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTTIFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISLSCENKIISFKENPPDNINKDTSKDIFFORSVPGHDNKKMFESSY 120
Db 61 AVTISVKCEKISLSCENKIISFKENPPDNINKDTSKDIFFORSVPGHDNKKMFESSY 120

QY 121 EGYFLACERDLFKLILKKEDELGDRSINFTVQNE 157
Db 121 EGYFLACERDLFKLILKKEDELGDRSINFTVQNE 157

RESULT 4
US-08-996-338-26
; Sequence 26, Application US/08996338
; Patent No. 6087116
; GENERAL INFORMATION:

APPLICANT: TORIGOE, Kakuji
APPLICANT: OKURA, Takanori
TITLE OF INVENTION: KURIMOTO, Masashi
TITLE OF INVENTION: WHICH INDUCES INTERFERON- PRODUCTION
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,338
FILING DATE: 22-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74,697/1997
FILING DATE: 12-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 215,488/1997
FILING DATE: 28-JUL-1997
APPLICATION DATA:
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 157
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-996-338-26

Query Match 99.4%; Score 810; DB 3; Length 157;
Best Local Similarity 99.4%; Pred. No. 7.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNAPRTFIISMYKDSQPRGM 60
DB 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNAPRTFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDKSDIIFQSVPGHDNKMQFESSY 120
DB 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDKSDIIFQSVPGHDNKMQFESSY 120
QY 121 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNEED 157

RESULT 5
US-08-558-818-1
Sequence 1, Application US/08558818
Patent No. 6197297
GENERAL INFORMATION:
APPLICANT: NAME-KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENKYUJO
APPLICANT: KUNIKATA, Toshio
APPLICANT: TANIGUCHI, Mutsuko
APPLICANT: KOHNO, Keizo

APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
TITLE OF INVENTION: WHICH INDUCES INTERFERON- PRODUCTION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: FELICIT-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/558,818
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: JP 58,240/95
PRIOR APPLICATION DATA: February 23, 1995
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-558-818-1

Query Match 99.4%; Score 810; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 7.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNAPRTFIISMYKDSQPRGM 60
DB 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNAPRTFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDKSDIIFQSVPGHDNKMQFESSY 120
DB 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDKSDIIFQSVPGHDNKMQFESSY 120
QY 121 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNEED 157

RESULT 6
US-08-974-469A-1
Sequence 1, Application US/08974469A
Patent No. 6207641
GENERAL INFORMATION:
APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENKYUJO
APPLICANT: TORIGOE, Kakuji
APPLICANT: TANIMOTO, Tadao
APPLICANT: FUKUDA, Shigeharu
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: AGENT FOR SUSCEPTIVE DISEASE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,469A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/599,879
FILING DATE:
APPLICATION NUMBER: JP 78,357/95
FILING DATE: March 10, 1995
APPLICATION NUMBER: JP 274,988/95
FILING DATE: September 29, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-469A-1

Query Match 99.4%; Score 810; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 7.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLVIRNLNDQVLFDQGNRPLFEDMTDSCRONAPRTIIFIISMYKDSQPRGM 60
DB 1 YFGKLESKLVIRNLNDQVLFDQGNRPLFEDMTDSCRONAPRTIIFIISMYKDSQPRGM 60
QY 61 AVTISVCKEISILSCENKIISFKEMNPPDNKDKSDIIFQKSVPGHDKMKQFESSY 120
DB 61 AVTISVCKEISILSCENKIISFKEMNPPDNKDKSDIIFQKSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 7
US-08-932-180-1
Sequence 1, Application US/08832180
Patent No. 6214584
GENERAL INFORMATION:
APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENKYUJO
APPLICANT: USHIO, Shimpel
APPLICANT: TORIGOE, Kakuji
APPLICANT: TANIMOTO, Tadao
APPLICANT: OKAMURA, Haruki
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: INTERFERON- PRODUCTION INDUCING
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA

ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,180
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/558,191
FILING DATE:
APPLICATION NUMBER: JP 304,203/94
FILING DATE: No. 6214584ember 15, 1994
APPLICATION NUMBER: 10048102
FILING DATE: September 18, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: USHIO-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-832-180-1

Query Match 99.4%; Score 810; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 7.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLVIRNLNDQVLFDQGNRPLFEDMTDSCRONAPRTIIFIISMYKDSQPRGM 60
DB 1 YFGKLESKLVIRNLNDQVLFDQGNRPLFEDMTDSCRONAPRTIIFIISMYKDSQPRGM 60
QY 61 AVTISVCKEISILSCENKIISFKEMNPPDNKDKSDIIFQKSVPGHDKMKQFESSY 120
DB 61 AVTISVCKEISILSCENKIISFKEMNPPDNKDKSDIIFQKSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 8
US-08-832-198-6
Sequence 6, Application US/08832198
Patent No. 6242255
GENERAL INFORMATION:
APPLICANT: AKITA, Kenji
APPLICANT: NUKADA, Yoshiyuki
APPLICANT: FUJII, Mitsukiyo
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk


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, PRIORITY APPLICATION DATA:
,
, APPLICATION NUMBER: JP 31,474/1997
, FILING DATE: 31-JAN-1997
, ATTORNEY/AGENT INFORMATION:
,
, NAME: BROWDY, ROGER L.
,
, REGISTRATION NUMBER: 25,618
, REFERENCE/DOCKET NUMBER: TANIMOTO-3
,
, TELECOMMUNICATION INFORMATION:
,
, TELEPHONE: 202-628-5197
,
, TELEFAX: 202-737-3528
,
, INFORMATION FOR SEQ ID NO: 2:
,
, SEQUENCE CHARACTERISTICS:
,
, LENGTH: 193 amino acids
,
, TYPE: amino acid
,
, STRANDEDNESS: single
,
, TOPOLOGY: linear
,
, MOLECULE TYPE: peptide
,
US-08-896-501A-2

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Query Match	99.4%; Score 810; DB 2; Length 193;
Best Local Similarity	99.4%; Pred. No. 9.8e-88;
Matches 156; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	1 YFGLESKLSVIRNLNDQVLFDIGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPGRM 60
Dd	37 YFGLESKLSVIRNLNDQVLFDIGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPGRM 96
QY	61 AVTTSVACEKIISLSCENKIISFRMNPDPNIKDTKSDIIFQRSPVGHDNKMQPSSSY 120
Dd	97 AVTTSVACEKIISLSCENKIISFRMNPDPNIKDTKSDIIFQRSPVGHDNKMQPSSSY 156
QY	121 EGYFLACEKERDLFKILKKDELDGDRSIMFTVNQNE 157
Dd	157 EGYFLACEKERDLFKILKKDELDGDRSIMFTVNQNE 193

RESULT 11
 US-08-832-180-9
 ; Sequence 9, Application US/08832180
 ; Patent No. 6214584
 ; GENERAL INFORMATION:
 ; APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
 ; APPLICANT: KENYUJO
 ; APPLICANT: USHIO, Shimpel
 ; APPLICANT: TORIGOE, kakuji
 ; APPLICANT: TANIMOTO, Tadao
 ; APPLICANT: OKAMURA, Haruki
 ; APPLICANT: KURIMOTO, Masashi
 ; TITLE OF INVENTION: INTERFERON- PRODUCTION INDUCING
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Broadway and Neimark
 ; STREET: 419 Seventh Street N.W. Ste. 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect Version 5.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/832.180
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/558,191
 ; FILING DATE:
 ; APPLICATION NUMBER: JP 304,203/94
 ; FILING DATE: No. 6214584ember 15, 1994

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; APPLICATION NUMBER: 10048102
; FILING DATE: September 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: USHIO-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-832-180-9

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Query Match 99.4%; Score 810; DB 4; Length 193;
Best Local Similarity 99.4%; Pred. No. 9.8e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLVSIRNLNQVLEIDOGNRPFLFEDMTDSDCRDNAPTIFIIISMYKDSQPRGM 60
| | | | |
Db 37 YFGKLESKLVSIRNLNQVLEIDOGNRPFLFEDMTDSDCRDNAPTIFIIISMYKDSQPRGM 96
| | | | |
Qy 61 AVTISVKCEKISILSCENKIISFKEMNPDPNIKDTKSIIFFQRSPVGHDNKMQPESSSY 120
| | | | |
Db 97 AVTISVKCEKISILSCENKIISFKEMNPDPNIKDTKSIIFFQRSPVGHDNKMQPESSSY 156
| | | | |
Qy 121 EGYFLACEKERDLFKLILKKDELGDRSIMFTVNQED 157
| | | | |
Db 157 EGYFLACEKERDLFKLILKKDELGDRSIMFTVNQED 193
| | | | |

RESULT 12
US-08-502-535B-2
Sequence 2, Application US/08502535B
Patent No. 5912324
GENERAL INFORMATION:
APPLICANT: OKAMURA, Haruki
APPLICANT: TANIMOTO, Tadao
APPLICANT: TORIGOE, Kakuji
APPLICANT: KUNIKATA, Toshio
APPLICANT: TANIGUCHI, Mutsuko
APPLICANT: KOHNO, Keizo
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: IFN-BETA PRODUCTION INDUCING PROTEIN AND
TITLE OF INVENTION: MONOCLONAL ANTIBODY OF THE SAME
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502,535B
FILING DATE: 14-JUL-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 184162/1994
FILING DATE: 14-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 45057/1995
FILING DATE: 10-FEB-1995

TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 157
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-996-338-27

Query Match 62.8%; Score 512; DB 3; Length 157;
Best Local Similarity 64.9%; Pred. No. 9.1e-53;
Matches 100; Conservative 26; Mismatches 26; Indels 2; Gaps 2;
QY 2 FGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGMA 61
Db 2 FGRUHCCTAVIRNLNDQVLFVDK-RQPVFEDMTDIDQASAPQTRLIIYMYKDSSEVRGLA 60
QY 62 VTISVKCEKISILSCENKIIISFKEMNPPDNIKDTKSDIIFFQSVPGHDKNMQFESSSYYE 121
Db 61 VTLVKDSKXSTLSCKNKKIISFEEMDPDENIDDIQSDLIFFQKRVPGH-NKMEFESSLYE 119
QY 122 GYFLACEKERDLFKLILKKEDELGDRSIMFTVQN 155
Db 120 GHFLACQKEDDAFKLILKKEDELGDRSIMFTLTN 153

RESULT 15

US-08-558-818-7
Sequence 7, Application US/08558818
Patent No. 6197297
GENERAL INFORMATION:

APPLICANT: NAME: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENKYUJO

APPLICANT: KUNIKATA, Toshio
APPLICANT: TANIGUCHI, Mutsuko
APPLICANT: KOHNO, Keizo
APPLICANT: KURIMOTO, Masashi

TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
TITLE OF INVENTION: WHICH INDUCES INTERFERON- PRODUCTION
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0

ATTORNEY/AGENT INFORMATION:

NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: FELICI-1

TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/558,818

FILING DATE:

CLASSIFICATION: 530
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: JP 58,240/95
PRIOR APPLICATION DATA: February 23, 1995

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 157 amino acids
TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: mouse
INDIVIDUAL ISOLATE: liver
US-08-558-818-7

Query Match 62.8%; Score 512; DB 4; Length 157;
Best Local Similarity 64.9%; Pred. No. 9.1e-53;
Matches 100; Conservative 26; Mismatches 26; Indels 2; Gaps 2;
QY 2 FGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGMA 61
Db 2 FGRUHCCTAVIRNLNDQVLFVDK-RQPVFEDMTDIDQASAPQTRLIIYMYKDSSEVRGLA 60
QY 62 VTISVKCEKISILSCENKIIISFKEMNPPDNIKDTKSDIIFFQSVPGHDKNMQFESSSYYE 121
Db 61 VTLVKDSKXSTLSCKNKKIISFEEMDPDENIDDIQSDLIFFQKRVPGH-NKMEFESSLYE 119
QY 122 GYFLACEKERDLFKLILKKEDELGDRSIMFTVQN 155
Db 120 GHFLACQKEDDAFKLILKKEDELGDRSIMFTLTN 153

Search completed: October 8, 2002, 10:14:17
Job time: 528 sec

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